

FoundationOne® Liquid CDx Technical Information

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FoundationOne® Liquid CDx Technical Information

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1 Intended Use

FoundationOne Liquid CDx is a qualitative next generation sequencing based *in vitro* diagnostic test that uses targeted high throughput hybridization-based capture technology to analyze 324 genes and report genomic alterations in 311 genes. These include substitutions, insertions and deletions (indels) in 311 genes, rearrangements in 8 genes and copy number alterations in 3 genes. FoundationOne Liquid CDx utilizes circulating cell-free DNA (cfDNA) isolated from plasma derived from anti-coagulated peripheral whole blood of cancer patients collected in FoundationOne Liquid CDx cfDNA blood collection tubes included in the FoundationOne Liquid CDx Blood Sample Collection Kit. The test is intended to be used as a companion diagnostic to identify patients who may benefit from treatment with the targeted therapies listed in **Table 1** in accordance with the approved therapeutic product labeling.

Table 1. Companion diagnostic indications

Tumor Type	Biomarker(s) Detected	Therapy
Breast cancer	<i>PIK3CA</i> mutations	ITOVEBI™ (inavolisib) in combination with palbociclib and fulvestrant
	<i>PIK3CA</i> mutations C420R, E542K, E545A, E545D [1635G>T only], E545G, E545K, Q546E, Q546R; and H1047L, H1047R, and H1047Y	PIQRAY® (alpelisib)
Colorectal cancer (CRC)	<i>BRAF</i> V600E	BRAFTOVI® (encorafenib) in combination with cetuximab
Non-small cell lung cancer (NSCLC)	<i>ALK</i> rearrangements	ALECENSA® (alectinib)
	<i>BRAF</i> V600E	BRAFTOVI® (encorafenib) in combination with MEKTOVI® (binimetinib)
	<i>EGFR</i> exon 19 deletions and <i>EGFR</i> exon 21 L858R substitution	EGFR tyrosine kinase inhibitors approved by FDA*
	<i>MET</i> single nucleotide variants (SNVs) and indels that lead to <i>MET</i> exon 14 skipping	TABRECTA® (capmatinib)
		TEPMETKO® (tepotinib)**
	<i>ROS1</i> fusions**	ROZLYTREK® (entrectinib)

Tumor Type	Biomarker(s) Detected	Therapy
Prostate cancer	<i>BRCA1, BRCA2, ATM</i> alterations	LYNPARZA® (olaparib)
	<i>BRCA1, BRCA2</i> alterations	AKEEGA® (niraparib + abiraterone acetate)
		LYNPARZA® (olaparib) in combination with abiraterone
		RUBRACA® (rucaparib)
	Homologous Recombination Repair (HRR) gene (<i>BRCA1, BRCA2, ATM, ATR, CDK12, CHEK2, FANCA, MLH1, MRE11A, NBN, PALB2, RAD51C</i>) alterations	TALZENNA® (talazoparib) in combination with XTANDI® (enzalutamide)
Solid tumors	<i>NTRK1/2/3</i> fusions**	ROZLYTREK® (entrectinib)

*For the most current information about the therapeutic products in this group, go to:

https://www.fda.gov/medical-devices/in-vitro-diagnostics/list-cleared-or-approved-companion-diagnostic-devices-in-vitro-and-imaging-tools#Group_Labeling

** When considering eligibility for ROZLYTREK® based on the detection of *NTRK1/2/3* and *ROS1* fusions or for TEPMETKO® based on the detection of *MET* SNVs and indels that lead to *MET* exon 14 skipping, testing using plasma specimens is only appropriate for patients for whom tumor tissue is not available for testing.

Additionally, FoundationOne Liquid CDx is intended to provide tumor mutation profiling to be used by qualified health care professionals in accordance with professional guidelines in oncology for patients with solid malignant neoplasms.

A negative result from a plasma specimen does not mean that the patient's tumor is negative for genomic findings. Patients with the tumor types above who are negative for the mutations listed in **Table 1** (see ** footnote under **Table 1** for *NTRK1/2/3* and *ROS1* fusions for ROZLYTREK® and *MET* SNVs and indels that lead to *MET* exon 14 skipping for TEPMETKO®) should be reflexed to routine biopsy and their tumor mutation status confirmed using an FDA-approved tumor tissue test, if feasible.

Genomic findings other than those listed in **Table 1** are not prescriptive or conclusive for labeled use of any specific therapeutic product.

~~FoundationOne Liquid CDx is performed at Foundation Medicine, Inc. owned and operated sites.~~

2 Contraindication

There are no known contraindications.

3 Warnings and Precautions

1. Alterations reported may include somatic (not inherited) or germline (inherited) alterations; however, the test does not distinguish between germline and somatic alterations. If a reported alteration is suspected to be germline, confirmatory testing should be considered in the appropriate clinical context.
2. The test is not intended to replace germline testing or to provide information about cancer predisposition.

3. Patients for whom no companion diagnostic alterations are detected should be considered for confirmation with an FDA-approved tumor tissue test, if possible.

4 Limitations

1. For *in vitro* diagnostic use only.
2. For prescription use only. This test must be ordered by a qualified medical professional in accordance with clinical laboratory regulations.
3. Genomic findings other than those listed in **Table 1** of the intended use are not prescriptive or conclusive for labeled use of any specific therapeutic product.
4. A negative result does not rule out the presence of an alteration in the patient's tumor.
5. Decisions on patient care and treatment must be based on the independent medical judgment of the treating physician, taking into consideration all applicable information concerning the patient's condition, such as patient and family history, physical examinations, information from other diagnostic tests, and patient preferences, in accordance with the standard of care in a given community.
6. The test is intended to be performed on specific serial number-controlled instruments by Foundation Medicine, Inc.
7. Genomic findings from cfDNA may originate from circulating tumor DNA fragments, germline alterations, or nontumor somatic alterations, such as clonal hematopoiesis of indeterminate potential (CHIP). Genes with alterations that may be derived from CHIP include, but are not limited to, the following: *ASXL1*, *ATM*, *CBL*, *CHEK2*, *DNMT3A*, *JAK2*, *KMT2D (MLL2)*, *MPL*, *MYD88*, *SF3B1*, *TET2*, *TP53*, and *U2AF1*. The efficacy of targeting such nontumor somatic alterations (e.g., CH) is unknown.
8. The analytical accuracy for the FoundationOne Liquid CDx assay has not been demonstrated in all genes.
9. The analytical accuracy for the FoundationOne Liquid CDx assay for the detection of SNVs and indels that lead to *MET* exon 14 skipping has not been demonstrated for samples with variant allele frequencies (VAF) below 0.34% for base substitutions and 0.73% VAF for small insertions and small deletions.
10. TABRECTA® efficacy has not been established in patients with *MET* SNVs <0.21% VAF and in patients with *MET* indels <0.16% VAF tested with FoundationOne Liquid CDx.
11. TEPMETKO® efficacy has not been established in patients with *MET* SNVs <0.19% VAF and in patients with *MET* indels <0.10% VAF tested with FoundationOne Liquid CDx.
12. ALECENSA® efficacy has not been established in patients with *ALK* rearrangements <0.06% VAF tested with FoundationOne Liquid CDx.
13. LYNPARZA® efficacy has not been established in prostate cancer patients with *BRCA1/2* or *ATM* rearrangements with <0.25% VAF or with short variants in *BRCA1/2* or *ATM* <0.11% VAF tested with FoundationOne Liquid CDx.

14. RUBRACA® efficacy has not been established in prostate cancer patients with *BRCA1/2* rearrangements with <0.85% VAF or with short variants in *BRCA1/2* <0.15% VAF tested with FoundationOne Liquid CDx.
 15. PIQRAY® efficacy has not been established in patients with *PIK3CA* SNVs with <0.14% VAF tested with FoundationOne Liquid CDx.
 16. BRAFTOVI® (encorafenib) in combination with cetuximab efficacy has not been established in patients with the *BRAF* V600E with <0.11 % VAF tested with FoundationOne Liquid CDx.
 17. BRAFTOVI® (encorafenib) in combination with MEKTOVI® (binimetinib) efficacy has not been established in patients with *BRAF* V600E with < 0.099% VAF tested with FoundationOneLiquid CDx.
 18. The precision of FoundationOne Liquid CDx was only confirmed for select variants at the limit of detection (LoD).
 19. The FoundationOne Liquid CDx assay does not detect heterozygous deletions.
 20. The FoundationOne Liquid CDx assay does not detect copy number losses/homozygous deletions in *ATM*, *ATR*, *CDK12*, *CHEK2*, *FANCA*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, and *RAD51C*. The prevalence of homozygous deletions in these genes ranges from 0-2.83% based on TALAPRO-2 trial data and 0-1.64% based on publicly available prostate cancer databases.
 21. A complete assessment of the impact of cfDNA blood collection tube lot-to-lot variability on the performance of the test has not been evaluated.
 22. The test is not intended to provide information on cancer predisposition.
- BRCA1/BRCA2* homozygous deletions and rearrangements were not adequately represented in all analytical studies.
23. Representation of *ALK* rearrangements were limited in the analytical validation studies.
 24. The representation of short variants and rearrangements in *ATM*, *ATR*, *CDK12*, *CHEK2*, *FANCA*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, and *RAD51C* was limited in the analytical validation studies.
 25. Performance has not been validated for cfDNA input below the specified minimum input.
 26. Representation of SNV and indels that lead to *MET* exon 14 skipping that represent biomarker rule category 1 and 2 (refer to Section 11.6 for the companion diagnostic biomarker definition), were limited in the analytical validation studies.
 27. For optimal ctDNA shed, it is recommended that blood be drawn prior to therapy or at a time of disease progression. The sensitivity of liquid biopsy is related to adequate levels of ctDNA shed. Therefore, assay performance will be dependent upon level of ctDNA shed at time of testing.
 28. Due to the low prevalence of *ROS1* fusions and *NTRK1/2/3* fusions, the positive predictive value (PPV) of the test (FoundationOne Liquid CDx positive, tissue negative) may be lower than reported in test labeling.
 29. FoundationOne Liquid CDx may miss a subset of patients with *NTRK1/2/3* fusion and *ROS1* fusion

positive solid tumors who may derive benefit from ROZLYTREK®. In a retrospective-prospective clinical study assessing concordance between FoundationOne Liquid CDx test results in plasma and patients whose tumor tissue tested positive and was the basis for enrollment into a clinical trial, the data demonstrated that the FoundationOne Liquid CDx test did not detect approximately 46% of potential responders with *NTRK1/2/3* fusions and 49% of responders with *ROS1* fusions.

30. ROZLYTREK® efficacy has not been established in patients with *NTRK2* fusions tested with FoundationOne Liquid CDx, given the low prevalence of the biomarker.
31. In a retrospective-prospective clinical study assessing concordance between FoundationOne Liquid CDx test results in plasma and patients whose tumor tissue tested positive and was the basis for enrollment into a clinical trial, FoundationOne Liquid CDx detected 1 of 7 different *NTRK3* fusion partners. Due to the rarity of these fusions, the accuracy of FoundationOne Liquid CDx for *NTRK3* fusions has not been adequately determined.
32. *NTRK2* fusions per the FoundationOne Liquid CDx biomarker rules for *NTRK1/2/3* fusions were not represented in analytical validation studies.
33. A study evaluating the concordance to a second method demonstrated that the agreement between FoundationOne Liquid CDx positive results and a comparator method for *NTRK1/3*, and *ROS1* was ≤ 50% (i.e., whether these are potential FoundationOne Liquid CDx false positives or false negatives by the comparator is unknown).
34. FoundationOne Liquid CDx may not detect a subset of patients with prostate cancer with *BRCA1/2* homozygous deletions who may derive benefit from AKEEGA. A subgroup analysis indicated that the FoundationOne Liquid CDx test did not detect approximately 81% (21/26) of prostate cancer patients with *BRCA1/2* homozygous deletions detected by FoundationOne CDx who derived benefit from AKEEGA. All samples were below the limit of detection for *BRCA2* copy number loss by the FoundationOne Liquid CDx assay. Additional testing to confirm the absence of *BRCA1/2* homozygous deletions in the patient's tumor tissue with another FDA approved test, if feasible, is strongly recommended. (Around 2.72% of patients with prostate cancer are expected to harbor *BRCA1/2* homozygous deletions, based on FMI internal data).
35. Results reported may include variants with very low variant allele frequency (SNVs <0.5% VAF and indels <1.0% VAF). Such alterations may be false positive results detected due to background signals inherent in sequencing methods designed for high sensitivity or due to clonal hematopoiesis of indeterminate potential (CHIP). Additional clinical investigation to confirm the presence of these variants in the patient's tumor with another FDA-approved or cleared test is strongly recommended.
36. *BRCA1/2* homozygous deletions may not be detected in a subset of prostate cancer patients by FoundationOne Liquid CDx. Additional testing to confirm the absence of *BRCA1/2* homozygous deletions in the patient's tumor tissue with another FDA approved test, if feasible, is strongly recommended.
37. FoundationOne Liquid CDx may miss a subset of patients with *MET* single nucleotide variants (SNVs) and indels that lead to *MET* exon 14 skipping alterations in NSCLC patients who may derive benefit from TEPMETKO®. In a retrospective clinical study assessing concordance between FoundationOne Liquid CDx test results in plasma and patients whose plasma or tumor tissue tested positive and was the basis for enrollment into a clinical trial, the data demonstrated that the FoundationOne Liquid CDx test did not detect approximately 33% of responders with *MET* single

nucleotide variants (SNVs) and indels that lead to *MET* exon 14 skipping alterations. Non-detection of *MET* exon 14 skipping alterations in these samples was attributed to low tumor fraction.

5 Test Principle

The FoundationOne Liquid CDx assay is performed exclusively at Foundation Medicine, Inc. owned and operated sites using circulating cfDNA isolated from plasma derived from anti-coagulated peripheral whole blood from patients with solid malignant neoplasms. The assay employs a single DNA extraction method to obtain cfDNA from plasma from whole blood. Extracted cfDNA undergoes whole-genome shotgun library construction and hybridization-based capture of 324 cancer-related genes. All coding exons of 309 genes are targeted; select intronic or non-coding regions are targeted in 15 of these genes (refer to **Table 2** for the complete list of genes interrogated by FoundationOne Liquid CDx). Hybrid-capture selected libraries are sequenced with deep coverage using the NovaSeq® 6000 platform. Sequence data are processed using a custom analysis pipeline designed to detect genomic alterations in 311 genes. These include base substitutions and indels in 311 genes, copy number alterations in 3 genes, and gene rearrangements in 8 genes. A subset of targeted regions in 75 genes is baited for enhanced sensitivity.

Table 2. The FoundationOne Liquid CDx assay interrogates 324 genes, including 309 genes with complete exonic (coding) coverage and 15 genes with only select non-coding coverage (indicated with an asterisk).

Select regions in 75 genes (indicated in bold) are captured with increased sensitivity. Genes are captured for increased sensitivity with complete exonic coverage unless otherwise noted.

ABL1 [Exons 4-9]	ACVR1B	AKT1 [Exon 3]	AKT2	AKT3	ALK [Exons 20-29, Introns 18,19]	ALOX12B	AMER1 (FAM123B)	APC	AR
ARAF [Exons 4, 5, 7, 11, 13, 15, 16]	ARFRP1	ARID1A	ASXL1	ATM	ATR	ATRX	AURKA	AURKB	AXIN1
AXL	BAP1	BARD1	BCL2	BCL2L1	BCL2L2	BCL6	BCOR	BCORL1	BCR* [Introns 8, 13, 14]
BRAF [Exons 11-18, Introns 7-10]	BRCA1 [Introns 2, 7, 8, 12, 16, 19, 20]	BRCA2 [Intron 2]	BRD4	BRIP1	BTG1	BTG2	BTK [Exons 2, 15]	C11orf30 (EMSY)	C17orf39 (GID4)
CALR	CARD11	CASP8	CBFB	CBL	CCND1	CCND2	CCND3	CCNE1	CD22
CD70	CD74* [Introns 6-8]	CD79A	CD79B	CD274 (PD-L1)	CDC73	CDH1	CDK12	CDK4	CDK6
CDK8	CDKN1A	CDKN1B	CDKN2A	CDKN2B	CDKN2C	CEBPA	CHEK1	CHEK2	CIC
CREBBP	CRKL	CSF1R	CSF3R	CTCF	CTNNA1	CTNNB1 [Exon 3]	CUL3	CUL4A	CXCR4
CYP17A1	DAXX	DDR1	DDR2 [Exons 5, 17, 18]	DIS3	DNMT3A	DOT1L	EED	EGFR [Introns 7, 15, 24-27]	EP300
EPHA3	EPHB1	EPHB4	ERBB2	ERBB3 [Exons 3, 6, 7, 8, 10, 12, 20, 21, 23, 24, 25]	ERBB4	ERCC4	ERG	ERRFI1	ESR1 [Exons 4-8]
ETV4* [Intron 8]	ETV5* [Introns 6, 7]	ETV6* [Introns 5, 6]	EWSR1* [Introns 7-13]	EZH2 [Exons 4, 16, 17, 18]	EZR* [Introns 9-11]	FAM46C	FANCA	FANCC	FANCG
FANCL	FAS	FBXW7	FGF10	FGF12	FGF14	FGF19	FGF23	FGF3	FGF4

FGF6	FGFR1 [Introns 1, 5, Intron 17]	FGFR2 [Intron 1, Intron 17]	FGFR3 [Exons 7, 9 (alternative designation exon 10), 14, 18, Intron 17]	FGFR4	FH	FLCN	FLT1	FLT3 [Exons 14, 15, 20]	FOXL2
FUBP1	GABRA6	GATA3	GATA4	GATA6	GNA11 [Exons 4, 5]	GNA13	GNAQ [Exons 4, 5]	GNAS [Exons 1, 8]	GRM3
GSK3B	H3F3A	HDAC1	HGF	HNF1A	HRAS [Exons 2, 3]	HSD3B1	ID3	IDH1 [Exon 4]	IDH2 [Exon 4]
IGF1R	IKBKE	IKZF1	INPP4B	IRF2	IRF4	IRS2	JAK1	JAK2 [Exon 14]	JAK3 [Exons 5, 11, 12, 13, 15, 16]
JUN	KDM5A	KDM5C	KDM6A	KDR	KEAP1	KEL	KIT [Exons 8,9,11,12, 13, 17, Intron 16]	KLHL6	KMT2A (MLL) [Introns 6, 8-11, Intron 7]
KMT2D (MLL2)	KRAS	LTK	LYN	MAF	MAP2K1 (MEK1) [Exons 2, 3]	MAP2K2 (MEK2) [Exons 2-4, 6, 7]	MAP2K4	MAP3K1	MAP3K13
MAPK1	MCL1	MDM2	MDM4	MED12	MEF2B	MEN1	MERTK	MET	MITF
MKNK1	MLH1	MPL [Exon 10]	MRE11A	MSH2 [Intron 5]	MSH3	MSH6	MST1R	MTAP	MTOR [Exons 19, 30, 39, 40, 43-45, 47, 48, 53, 56]
MUTYH	MYB* [Intron 14]	MYC [Intron 1]	MYCL (MYCL1)	MYCN	MYD88 [Exon 4]	NBN	NF1	NF2	NFE2L2
NFKBIA	NKX2-1 (TTF-1)	NOTCH1	NOTCH2 [Intron 26]	NOTCH3	NPM1 [Exons 4-6, 8, 10]	NRAS [Exons 2, 3]	NSD3 (WHSC1L1)	NT5C2	NTRK1 [Exons 14, 15, Introns 8-11]
NTRK2 [Intron 12]	NTRK3 [Exons 16, 17]	NUTM1* [Intron 1]	P2RY8	PALB2	PARK2	PARP1	PARP2	PARP3	PAX5
PBRM1	PDCD1 (PD-1)	PDCD1LG2 (PD-L2)	PDGFRA [Exons 12, 18, Introns 7, 9, 11]	PDGFRB [Exons 12-21, 23]	PDK1	PIK3C2B	PIK3C2G	PIK3CA [Exons 2, 3, 5-8, 10, 14, 19, 21 (Coding Exons 1, 2, 4-7, 9, 13, 18, 20)]	PIK3CB
PIK3R1	PIM1	PMS2	POLD1	POLE	PPARG	PPP2R1A	PPP2R2A	PRDM1	PRKAR1A
PRKCI	PTCH1	PTEN	PTPN11	PTPRO	QKI	RAC1	RAD21	RAD51	RAD51B
RAD51C	RAD51D	RAD52	RAD54L	RAF1 [Exons 3, 4, 6, 7, 10, 14, 15, 17, Introns 4-8]	RARA [Intron 2]	RB1	RBM10	REL	RET [Introns 7, 8, Exons 11, 13-16, Introns 9-11]
RICTOR	RNF43	ROS1 [Exons 31, 36-38, 40, Introns 31-35]	RPTOR	RSPO2* [Intron 1]	SDC4* [Intron 2]	SDHA	SDHB	SDHC	SDHD
SETD2	SF3B1	SGK1	SLC34A2* [Intron 4]	SMAD2	SMAD4	SMARCA4	SMARCB1	SMO	SNCAIP

<i>SOCS1</i>	<i>SOX2</i>	<i>SOX9</i>	<i>SPEN</i>	<i>SPOP</i>	<i>SRC</i>	<i>STAG2</i>	<i>STAT3</i>	<i>STK11 (LKB1)</i>	<i>SUFU</i>
<i>SYK</i>	<i>TBX3</i>	<i>TEK</i>	<i>TERC*</i> {ncRNA}	<i>TERT*</i> {Promoter}	<i>TET2</i>	<i>TGFBR2</i>	<i>TIPARP</i>	<i>TMPRSS2*</i> [Introns 1-3]	<i>TNFAIP3</i>
<i>TNFRSF14</i>	<i>TP53</i>	<i>TSC1</i>	<i>TSC2</i>	<i>TYRO3</i>	<i>U2AF1</i>	<i>VEGFA</i>	<i>VHL</i>	<i>WHSC1</i>	<i>WT1</i>
<i>XPO1</i>	<i>XRCC2</i>	<i>ZNF217</i>	<i>ZNF703</i>						

The classification criteria for all companion diagnostic (CDx) variants are outlined at the end of this document. The output of the test includes:

Category 1: CDx claims noted in **Table 1** of the Intended Use

Category 2: cfDNA Biomarkers with Strong Evidence of Clinical Significance in cfDNA

Category 3: Biomarkers with Evidence of Clinical Significance in tissue supported by:

3A: strong analytical validation using cfDNA

3B: analytical validation using cfDNA

Category 4: Other Biomarkers with Potential Clinical Significance

As part of its FDA-approved intended use, copy number alterations and rearrangements are reported in the genes listed in **Table 3**.

Table 3. Genes for which copy number alterations and rearrangements are reported for tumor profiling by FoundationOne Liquid CDx

Alteration Type	Genes
Copy Number Alterations	<i>BRCA1, BRCA2, ERBB2</i>
Rearrangements	<i>ALK, BRCA1, BRCA2, NTRK1, NTRK2, NTRK3</i>

6 FoundationOne Liquid CDx cfDNA Blood Specimen Collection Kit Contents

Test Kit Contents

The test includes a sample shipping kit, which is sent to ordering laboratories and physicians. The shipping kit contains the following components:

1. Specimen preparation and shipping instructions
2. Two FoundationOne Liquid CDx cfDNA blood collection tubes (8.5 mL nominal fill volume per tube)
3. Return shipping label

All other reagents, materials and equipment needed to perform the assay are used exclusively in the Foundation Medicine laboratory. The FoundationOne Liquid CDx assay is intended to be performed with serial number-controlled instruments.

7 FoundationOne Liquid CDx Test Ordering

To order FoundationOne Liquid CDx, the test order form in the test kit must be fully completed and signed by the ordering physician or other authorized medical professional. Please refer to Specimen Preparation Instructions and Shipping Instructions included in the test kit.

8 Instruments

The FoundationOne Liquid CDx device is intended to be performed with the following instruments, as identified by specific serial numbers:

9 Performance Characteristics

Performance characteristics were established using contrived and clinical circulating cfDNA derived from blood specimens extracted from a wide range of tumor types. **Table 4** below provides a summary of the number of tumor types and variants included in each study. As summarized in this table, each study included a broad range of representative alteration types (substitutions, insertions and deletions, rearrangements, and copy number alterations) in various genomic contexts across a number of genes. The validation studies included >7,000 sample replicates, >31,000 unique variants [includes variants classified as variants of unknown significance (VUS) and/or benign], and >30 tumor types, representing all 324 genes targeted by the FoundationOne Liquid CDx assay.

Table 4. Representation of tumor types and variants¹ across validation studies

Study Title	Cancer Types Represented	# Unique Samples	# of Sample Replicates	# of Unique Genes	# of Unique				
					Subs	Indels	Rearrang.	Copy Number Amplif.	Copy Number Losses
Contrived Sample Functional Characterization (CSFC) Study	Breast cancer Colorectal cancer Lung cancer Contrived samples	13	1843	228	563	81	11	1	1
FoundationOne Liquid CDx to Validated NGS Tumor Tissue Test Concordance: <i>BRCA1</i> and <i>BRCA2</i> Variants	Prostate cancer Ovarian cancer	279	N/A	2	100	87	9	0	2
FoundationOne Liquid CDx to Validated NGS cfDNA Assay Concordance: <i>PIK3CA</i> mutations	Breast cancer	412	N/A	1	32	5	0	0	0
Orthogonal Concordance	23 cancer types Contrived samples	278	N/A	64	541	12	11	3	0
LoD Estimation	Prostate Contrived samples	10	877	286	1490	247	32	13	3
LoB Study 1	Healthy Donors	28	79	322	26134	4482	911	222	42
LoB Study 2 ³	Healthy Donors	44	131	532	29507	4438	2752	222	42
Potentially Interfering Substances	Contrived samples	9	336	18	16	11	11	1	2
Hybrid Capture Bait Specificity	25 cancer types Contrived samples	3546	N/A	324	N/A	N/A	N/A	N/A	N/A
Reagent Stability	Contrived samples	8	142	279	1090	215	32	17	2
Reagent Interchangeability	Contrived samples	8	192	20	15	11	11	1	1

Study Title	Cancer Types Represented	# Unique Samples	# of Sample Replicates	# of Unique Genes	# of Unique				
					Subs	Indels	Rearrang.	Copy Number Amplif.	Copy Number Losses
Platform Precision study 1	Breast cancer Colon cancer Lung cancer Ovarian cancer Prostate cancer Skin cancer Contrived samples	47	1121	280	900	229	63	49	5
Platform Precision study 2	Lung cancer Prostate cancer Stomach cancer Colorectal cancer Bile duct cancer Breast cancer	10	230	6	6	4	0	0	0
Precision of detection of SNVs and indels that lead to <i>MET</i> exon 14 skipping (Precision study 3)	Lung Cancer	5	166	1	2	3	N/A	N/A	N/A
Platform Precision study 4 ³	Ovarian cancer Prostate cancer Breast cancer Lung cancer Colon adenocarcinoma Soft tissue neuroblastoma	17	402	159	258	43	6	22	1
DNA Extraction	Colorectal cancer Prostate cancer Breast cancer Lung cancer Skin cancer	6	72	161	265	53	2	0	0
Whole Blood Sample Stability	Lung cancer Colorectal cancer Gastrointestinal (non-Colorectal cancer) Prostate cancer Breast cancer Ovarian cancer	74	148	206	490	76	12	14	0
Inverted Tube Whole Blood Sample Stability	Lung cancer Colorectal cancer Breast cancer Ovarian cancer Prostate cancer	156	312	280	1295	195	19	27	0
Cross Contamination	Contrived samples	5	376	39	9	5	4	21	1
Guard Banding	Contrived samples	10	375	20	17	12	12	1	1
Guard Banding with updated LC input ³	Contrived samples	7	105	22	16	11	6	1	1
Clinical validation for detection of <i>EGFR</i> exon 19 deletions and L858R alterations: non-inferiority study ²	Lung cancer	177	N/A	1	5	7	N/A	N/A	N/A

Study Title	Cancer Types Represented	# Unique Samples	# of Sample Replicates	# of Unique Genes	# of Unique				
					Subs	Indels	Rearrang.	Copy Number Amplif.	Copy Number Losses
Clinical validation study for detection of deleterious alterations in <i>BRCA1</i> and <i>BRCA2</i> in prostate cancer ²	Prostate cancer	199	N/A	2	44	55	8	0	1
Clinical validation study for the detection of deleterious alterations in <i>BRCA1</i> and <i>BRCA2</i> in prostate cancer	Prostate Carcinoma	396	N/A	2	44	77	7	N/A	1
Clinical validation study for detection of <i>PIK3CA</i> mutations in breast cancer ²	Breast	359	N/A	1	28	4	0	0	0
Clinical validation study for <i>ALK</i> rearrangements in NSCLC ²	Lung cancer	249	N/A	1	13	1	11	1	0
Clinical validation study for <i>BRCA1</i> , <i>BRCA2</i> , and <i>ATM</i> alterations in prostate cancer ²	Prostate cancer	333	N/A	3	48	75	10	0	1
Clinical validation study for detection of SNVs and indels that lead to <i>MET</i> exon 14 skipping ²	Lung Cancer	171 ²	N/A	1	10	22	N/A	N/A	N/A
Clinical validation study for detection of SNVs and indels that lead to <i>MET</i> exon 14 skipping ²	Lung Cancer	241	N/A	1	11	45	N/A	N/A	N/A
Clinical validation study for detection of rearrangements that lead to <i>NTRK</i> fusions ²	Solid Tumor	203	N/A	14	N/A	N/A	12	N/A	N/A
Clinical validation study for detection of rearrangements that lead to <i>ROS1</i> fusions ²	Lung Cancer	203	N/A	8	N/A	N/A	7	N/A	N/A
Clinical validation study for detection of <i>BRAF</i> V600E in CRC	Colorectal Cancer	433	N/A	1	1	0	0	0	0
Clinical validation study for detection <i>BRAF</i> V600E in NSCLC	Lung Cancer	218	N/A	1	1	N/A	N/A	N/A	N/A

Study Title	Cancer Types Represented	# Unique Samples	# of Sample Replicates	# of Unique Genes	# of Unique				
					Subs	Indels	Rearrang.	Copy Number Amplif.	Copy Number Losses
Clinical validation study for detection of <i>PIK3CA</i> short variants in breast cancer	Breast Cancer	268	N/A	1	21	N/A	N/A	N/A	N/A
Clinical validation study for detection of HRR gene alterations (<i>BRCA1</i> , <i>BRCA2</i> , <i>ATM</i> , <i>ATR</i> , <i>CDK12</i> , <i>CHEK2</i> , <i>FANCA</i> , <i>MLH1</i> , <i>MRE11A</i> , <i>NBN</i> , <i>PALB2</i> , <i>RAD51C</i>) in Prostate cancer	Prostate Cancer	399	N/A	12	141	216	13	0	1
Blood Collection Tube Equivalence	Ovarian cancer Breast cancer Colorectal cancer Prostate cancer Lung cancer Skin cancer Stomach cancer	60	192	116	135	39	13	5	0
Automation Line Equivalence	Contrived samples	8	187	303	1926	337	63	61	4
Updated LC Method Comparison Study ³	10 cancer types	81	324	338	4220	364	148	116	2
Variant Report Curation	Breast cancer Colorectal cancer Lung cancer Prostate cancer Skin cancer	19	57	183	300	104	15	11	2
Pan-tumor performance (includes historical analysis)	20 cancer types	19868	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Molecular Index Barcode Performance	25 cancer types Contrived samples	7637	N/A	324	N/A	N/A	N/A	N/A	N/A
FoundationOne Liquid LDT to FoundationOne Liquid CDx Concordance	25 cancer types	927	N/A	73	1815	376	109	46	N/A
FoundationOne Liquid CDx to Validated cfDNA NGS Assay Concordance: <i>MET</i> exon 14 (Primary Analysis)	Lung Cancer	172	N/A	1	11	21	N/A	N/A	N/A
FoundationOne Liquid CDx to Validated cfDNA NGS Assay Concordance: <i>NTRK</i> fusions ⁴	Solid Tumor	116	N/A	5	N/A	N/A	4	N/A	N/A

Study Title	Cancer Types Represented	# Unique Samples	# of Sample Replicates	# of Unique Genes	# of Unique				
					Subs	Indels	Rearrang.	Copy Number Amplif.	Copy Number Losses
Precision and LoD Confirmation of <i>NTRK</i> Gene Fusions in a Pan-tumor Setting ⁴	Solid Tumor	4	93	6	N/A	N/A	4	N/A	N/A
FoundationOne Liquid CDx to Validated cfDNA NGS Assay Concordance: <i>EGFR</i> exon 20 insertions	Lung Cancer	151	N/A	1	N/A	25	N/A	N/A	N/A
Precision and LoD Confirmation of <i>EGFR</i> exon 20 insertions	Lung Cancer	3	72	1	N/A	3	N/A	N/A	N/A
FoundationOne Liquid CDx to Validated cfDNA NGS Assay Concordance: <i>BRAF</i> V600E	Colorectal Cancer NSCLC	304	608	1	1	N/A	N/A	N/A	N/A
Precision and Confirmation of LoD of <i>BRAF</i> V600E	Colorectal Cancer	1	24	1	1	N/A	N/A	N/A	N/A
Precision and Confirmation of LoD of <i>BRAF</i> V600E	NSCLC	1	22	1	1	N/A	N/A	N/A	N/A
Precision and Confirmation of LoD of HRR gene alterations (<i>BRCA1</i> , <i>ATR</i> , <i>CDK12</i> , <i>CHEK2</i> , <i>FANCA</i> , <i>MLH1</i> , <i>MRE11A</i> , <i>NBN</i> , <i>PALB2</i> , <i>RAD51C</i>)	Prostate Cancer, Colorectal Cancer	19	672	10	4	7	8	N/A	1
FoundationOne Liquid CDx to Validated cfDNA NGS Assay Concordance: HRR gene alterations (<i>ATR</i> , <i>CDK12</i> , <i>CHEK2</i> , <i>FANCA</i> , <i>MLH1</i> , <i>MRE11A</i> , <i>NBN</i> , <i>PALB2</i> , and <i>RAD51C</i>)	Prostate Cancer	163	N/A	9	40	76	N/A	N/A	N/A

¹Variants detected may include variants classified as VUS and benign.

²Clinical validation study was conducted using the original LC input range for FoundationOne Liquid CDx (30ng-80ng, with conditional processing of samples between 20-30ng)

³Study was conducted to validate the new LC input range for FoundationOne Liquid CDx (20ng-60ng). LDT = Laboratory Developed Test

9.1 Concordance – Comparison to an Orthogonal cfDNA NGS Method #1

The detection of short variants and rearrangements by the FoundationOne Liquid CDx assay was compared to that of an externally validated cfDNA next generation sequencing (NGS) assay in 74 genes common to both assays across 278 samples that represented an array of tumor types (>50 unique disease ontologies across 23 cancer types). The cancer types (# samples) included lung [NSCLC (75) and other (3)]; breast (54); prostate (32); colorectal [colon (27) and rectal (6)]; liver (11); ovarian (6);

pancreas (9); gastrointestinal (7); bile duct (2); esophageal (5); skin (6); cervical (1); anal (1); bladder (1); gallbladder (1); salivary gland (2); thymus (1); thyroid (3); uterine (2); fallopian tube (1); head and neck (1); soft tissue (1); and unknown primary (19). The study included samples selected from clinical FoundationOne Liquid testing (n=268) and contrived samples consisting of fragmented gDNA diluted in clinical cfDNA to represent rare alterations (n=10).

Using the externally validated NGS assay as the comparator, the analysis demonstrated a short variant positive percent agreement (PPA) of 96.2% with a 95% two-sided confidence interval (CI) of [94.8%-97.4%]. The short variant negative percent agreement (NPA) was >99.9% with a 95% two-sided CI of [99.9%-100.0%]. The respective PPA of base substitutions and indels with a 95% two-sided CI was 96.1% [94.6%-97.3%] and 100.0% [85.2%-100.0%]. The respective NPA and 95% two-sided CI of base substitutions and indels was >99.9% [99.9%-100.0%] and 100.0% [99.89%-100.0%] (**Table 5**).

Table 5. Concordance of short variants called in FoundationOne Liquid CDx and the cfDNA comparator assay (n= 902 positive variants, n= 152,832 negative variants* by the comparator assay)

Variant Type	FoundationOne Liquid CDx(+) Comparator(+)	FoundationOne Liquid CDx(-) Comparator(+)	FoundationOne Liquid CDx(+) Comparator(-)	FoundationOne Liquid CDx(-) Comparator(-)	PPA [95% CI]	NPA [95% CI]	OPA [95% CI]
All Short Variants	868	34	8	152824	96.2% [94.8%-97.4%]	>99.9% [99.9%-100.0%]	>99.9% [99.9%-100.0%]
Base Substitutions	845	34	8	149511	96.1% [94.6%-97.3%]	>99.9% [99.9%-100.0%]	>99.9% [99.9%-100.0%]
Indels	23	0	0	3313	100.0% [85.2%- 100.0%]	100.0% [99.9%- 100.0%]	100.0% [99.9%- 100.0%]

* Variants detected include variants classified as VUS and benign.

For the concordance of rearrangement detection between FoundationOne Liquid CDx and the comparator assay, the observed rearrangement PPA was 100.0%, with a 95% two-sided CI of [59.0%-100.0%]. The NPA was 99.8%, with a 95% two-sided CI [99.5%-100.0%] (**Table 6**).

Table 6. Concordance of rearrangements called in FoundationOne Liquid CDx and the cfDNA comparator assay (n= 7 positive, n=1685 negative* as determined by the comparator assay)

	Comparator (+)	Comparator (-)	Total
FoundationOne Liquid CDx (+)	7	3	10
FoundationOne Liquid CDx (-)	0	1682	1682
Total	7	1685	1692
	PPA: 100.0% [59.0% - 100.0%]	NPA: 99.8% [99.5% - 100.0%]	OPA: 99.8% [99.5% - 100.0%]

* Variants detected include variants classified as VUS and benign.

Assessment of a subset of highly-actionable alterations were compared between the two assays. The analysis resulted in a PPA of 100% across all eligible highly-actionable alterations called in the comparator assay (**Table 7**).

Table 7. Concordance of CDx alterations called between FoundationOne Liquid CDx and the comparator assay (n = 78)

Targeted Alteration	n	PPA [95% CI]	NPA [95% CI]	PPV [95% CI]	NPV ¹ [95% CI]
ALK rearrangements*	1	100% [2.5%-100%]	99.9% [99.7%-100%]	50% [1.3%-98.7%]	100% [99.3%-100%]
BRCA1 short variants*	1	100% [2.5%-100%]	100% [98.7%-100%]	100% [2.5%-100%]	100% [98.7%-100%]
BRCA2 short variants*	2	100% [15.8%-100%]	100% [99.3%-100%]	100% [15.8%-100%]	100% [99.3%-100%]
EGFR exon 19 deletions*	11	100% [71.5%-100%]	100% [99.7%-100%]	100% [71.5%-100%]	100% [99.7%-100%]
EGFR L858R*	10	100% [69.2%-100%]	100% [98.7%-100%]	100% [69.2%-100%]	100% [98.7%-100%]
NTRK1 rearrangements*	3	100% [29.2%-100%]	100% [99.8%-100%]	100% [29.2%-100%]	100% [99.3%-100%]
PIK3CA base substitutions*	49	100% [92.7%-100%]	100% [99.9%-100%]	100% [92.7%-100%]	100% [99.9%-100%]
ROS1 rearrangements*	1	100% [20.7%-100%]	99.6% [98.0%-99.9%]	50% [9.5%-90.6%]	100% [98.6%-100%]

*The PPA and NPA for these alterations are unadjusted

¹Negative Predictive Value (NPV)

These data demonstrate that the FoundationOne Liquid CDx assay and an externally-validated NGS assay are highly concordant across the 76 genes common between the two panels.

9.2 Concordance – FoundationOne Liquid CDx to validated NGS tumor tissue assay (BRCA1 and BRCA2 alterations)

Samples from a total of 279 prostate and ovarian cancer patients were tested and the concordance evaluated between FoundationOne Liquid CDx and the validated NGS tumor tissue assay for the detection of deleterious alterations in *BRCA1* or *BRCA2*. As summarized below, a PPA of 88.03% and an NPA of 95.68% were observed on a sample level (**Table 8**). As summarized in **Table 9** an overall PPA of 87.28% and an NPA of 99.83% were observed at the variant level. Some discordance is expected based on biological differences and sampling times between tumor tissue and plasma samples. Considering the impact of biological differences between analytes, these data demonstrate a high concordance between FoundationOne Liquid CDx and the validated NGS tumor tissue assay for the detection of deleterious alterations in *BRCA1* or *BRCA2*.

Table 8. Concordance (by sample) of FoundationOne Liquid CDx and validated NGS tumor tissue assay in prostate and ovarian cancer patients for the detection of alterations in BRCA1 or BRCA2

		NGS Tumor Tissue Assay	
		Positive	Negative
FoundationOne Liquid CDx	Positive	103	7
	Negative	14	155
		PPA: 88.03% [80.91%-92.74%]	NPA: 95.68% [91.35%-97.89%]

Table 9. Concordance (by variant) of FoundationOne Liquid CDx and validated NGS tumor tissue assay in prostate and ovarian cancer patients for the detection of alterations in BRCA1 or BRCA2

	F1LCDx+ /Tissue+	F1LCDx- /Tissue+	F1LCDx+ /Tissue-	F1LCDx-/ Tissue-	PPA (95% CI)	NPA (95% CI)
Substitutions	77	6	29	20255	92.77% (85.11%, 96.64%)	99.86% (99.79%, 99.90%)
Indels	65	3	31	16362	95.59% (87.81%, 98.49%)	99.81% (99.73%, 99.87%)
Rearrangements	4	3	7	1939	57.14% (25.05%, 84.18%)	99.64% (99.26%, 99.83%)
Copy number loss	5	10	1	263	33.33% (15.18%, 58.29%)	99.62% (97.89%, 99.93%)
Total	151	22	68	38819	87.28% (81.50%, 91.45%)	99.83% (99.78%, 99.86%)

9.3 Concordance – Comparison to an Orthogonal cfDNA NGS Method #2

The accuracy of using FoundationOne Liquid CDx as a companion diagnostic to identify breast cancer patients harboring *PIK3CA* alterations was assessed with residual plasma samples from the SOLAR-1 clinical trial. Of the remaining plasma samples, 542 were evaluable by the externally-validated NGS method and produced valid results. 418 were evaluable by FoundationOne Liquid CDx, of which 192 positive variants were detected across 188 patients, with 4 patients possessing 2 positive variants each. The distribution of counts per positive variant is listed in **Table 10**.

Table 10. Distribution of variants detected with FoundationOne Liquid CDx evaluable samples.

Protein Effect in <i>PIK3CA</i>	# Variant Calls (188 Positive Samples)
C420R	3
E542K	25
E545A	1
E545G	2
E545K	50
H1047L	9
H1047R	100
H1047Y	1
Q546R	1
Total	192

A total of 412 valid samples generated valid results with both assays. The primary analysis using NGS Method #2 as the reference assay achieved a PPA [95% CI] of 97.06% [93.27%, 99.04%], and an NPA [95% CI] of 91.74% [87.52%, 94.88%]. The contingency table for this comparison is provided in **Table 11**, with counts representing number of samples (versus number of variant calls).

The sample counts in the core 2x2 white boxes total to 412 samples. There were seven samples evaluable with FoundationOne Liquid CDx but failed (italicized in **Table 11**), as well as three samples missing from reference assay data. There were five samples unevaluable by the reference assay; three

of these aligned with the 418 evaluable FoundationOne Liquid CDx samples, while two were among the 130 samples not evaluable due to insufficient plasma.

Table 11. Contingency table comparing FoundationOne Liquid CDx with the reference assay, primary analysis with 412 cases.

		Reference Assay					
		Positive	Negative	Not Evaluable	Missing	Total	
FoundationOne Liquid CDx	Positive	165	20	2	1	188	PPA _{F1L} : 89.19% [83.80%, 93.27%]
	Negative	5	222	1	2	230	NPA _{F1L} : 97.80% [94.93%-99.28%]
	Evaluable but Failed	0	7	0	0	7	
	Not Evaluable	35	93	2	0	130	
	Total	205	342	5	3	555	
		PPA _{ONC} : 97.06% [93.27%, 99.04%]	NPA _{ONC} : 91.74% [87.52%, 94.88%]				OPA: 93.93% [91.17%, 96.04%]

9.4 Concordance – FoundationOne Liquid CDx to an externally validated cfDNA NGS assay (SNVs and indels that lead to MET exon 14 skipping)

An analytical accuracy study was performed to demonstrate the concordance between FoundationOne Liquid CDx and an externally validated cfDNA NGS comparator (evNGS) assay for the detection of SNVs and indels that lead to *MET* exon 14 skipping. Overall, there were 74 overlapping genes targeted by the 2 assays and the comparator assay bait set covered the same regions as the FoundationOne Liquid CDx bait set.

The analytical accuracy study was conducted with 45 samples from the clinical bridging study with 41 samples from patients enrolled in the GEOMETRY-mono 1 trial (refer to Section 10.7 below). An additional 100 NSCLC samples were sourced from Foundation Medicine's clinical archives, 38 samples from NSCLC patients previously evaluated in the accuracy study to support the original PMA P190032 (refer to section 9.1 above) and 31 externally sourced plasma samples from NSCLC cases whose tissue specimens tested positive for *MET* exon 14 skipping alterations and were subsequently tested with FoundationOne Liquid CDx to determine their *MET* exon 14 skipping associated alteration status prior to conducting the accuracy study statistical analysis. Samples selected from Foundation Medicine's clinical archives that were positive for *MET* exon 14 skipping alterations had to have a variant allele frequency (VAF) greater than or equal 0.40%.

Of the 214 samples, 179 samples had DNA yield that allowed processing with FoundationOne Liquid CDx at the specified LC DNA input of 30ng-80ng. Thirty-five (35) samples were tested with FoundationOne Liquid CDx at a lower LC DNA input of out of specification of 20ng-<30ng LC DNA input. Of the 179 samples that had sufficient DNA yield for testing with FoundationOne Liquid CDx, 3 samples had a FoundationOne Liquid CDx sequence analysis Quality Control (QC) failure, while 4 had an evNGS QC failure.

The primary analytical concordance analysis, using the evNGS assay results as the reference, included 172 samples that passed QC with both assays. Forty-eight (48) of the 172 samples were identified as positive for *MET* exon 14 skipping alterations by FoundationOne Liquid CDx. The statistical analysis using the evNGS assay results as the reference showed a PPA of 94.87% with 95% CI (83.11%-98.58%), a NPA of 91.83% with 95% CI (85.80%, 95.32%), a PPV of 77.08% with 95% CI (63.46%,

86.69%) and a negative predictive value (NPV) of 98.39% with 95% CI (94.31%, 99.56%) as shown in **Table 12**. Since the samples were selected from different sources based on different assays, the unadjusted PPA/NPA and unadjusted PPV/NPV in **Table 12** may be subject to potential bias.

Table 12. Primary Concordance Analysis Comparing Sample-level Biomarker Detection between FoundationOne Liquid CDx and Comparator Assay

		evNGS			
		<i>MET</i> ex14 positive	<i>MET</i> ex14 negative	Total	PPV/NPV (95% CI)
F1LCDx	<i>MET</i> ex14 positive	37	11	48	PPV: 77.08% (63.46%, 86.69%)
	<i>MET</i> ex14 Negative	2	122	124	NPV: 98.39% (94.31%, 99.56%)
	Total	39	133	172	
	PPA/NPA (95% CI)	PPA: 94.87% (83.11%, 98.58%)	NPA: 91.83% (85.80%, 95.32%)		

Ten (10) of the eleven (11) samples that were F1LCDx-positive/evNGS-negative [F1LCDx(+)/evNGS(-)] were discordant due to differences in variant reporting by assays. Of the 11 samples, 10 samples harbored *MET* exon 14 deletions ≥ 6 bp detectable by the evNGS variant caller, which calls variants in the evNGS's loci of interest (LOI) and indels ≥ 6 bp in *MET* exon 14. Since *MET* ex14 indels ≥ 6 bp are not part of the evNGS's LOI, this variant type is filtered out and not reported by the evNGS's analysis software in the default setting, and thus are considered negatives by the evNGS comparator assay. Further the remaining one (1) sample from the 11 samples that were F1LCDx(+)/evNGS(-), contained a *MET* exon 14 deletion < 6 bp which cannot be called with the evNGS variant because the variant caller can only output *MET* exon 14 deletions ≥ 6 bp. The evNGS reporting rules only correspond to biomarker rule category 3, so all 37 samples that were F1LCDx(+)/evNGS(+) had *MET* exon 14 skipping alterations that correspond to biomarker rule category 3, i.e., these samples had base substitutions and indels affecting positions 0, +1, +2, or +3 at the splice donor site of the 3' boundary of *MET* exon 14. The evNGS assay does not call category 1 and 2 biomarkers as they are not included in their LOI. In the two discordant samples that were F1LCDx-negative(-)/evNGS(+), base substitutions reported by the evNGS were not detected in the variant analysis pipeline of FoundationOne Liquid CDx.

Four of the eleven discordant samples that were F1LCDx(+)/evNGS(-) were from patients evaluated in the clinical therapeutic study for whom efficacy data was available. Of these 4 patients, 3 had partial response to TABRECTA, while one had progressive disease. Although these patients had discordant results, these results appear to suggest that these patient with F1LCDx(+)/evNGS(-) were *MET* exon 14 deletion positive.

9.5 Concordance – FoundationOne Liquid CDx to an externally validated cfDNA NGS assay (NTRK1/2/3 Fusions)

An analytical accuracy study was performed to demonstrate the concordance between FoundationOne Liquid CDx and an externally validated cfDNA NGS comparator assay for the detection of *NTRK* fusions. For this study, seven (7) residual cfDNA samples were selected from patients enrolled in the STARTRK-2 trial used to support the effectiveness of the device, seven (7) residual cfDNA clinical samples were externally sourced, and 102 residual cfDNA samples were sourced from Foundation Medicine's clinical archives. Overall, a total of 116 sample replicates were processed using FoundationOne Liquid CDx in this study. Of the 116 samples, 113 were processed with the evNGS. Of the 113 samples run by both assays for this study, one (1) sample had a FoundationOne Liquid CDx post-sequencing QC failure, while 10 had an evNGS post-sequencing QC failure.

Measures of analytical concordance for the 102 samples that passed QC with both assays were determined. Since specimens were selected based on FoundationOne Liquid CDx and confirmed by the evNGS agreement, PPV and NPV are estimated conditional on FoundationOne Liquid CDx. PPV was estimated as 40% (4/10) with two-sided 95% CI (16.8%, 68.7%), and NPV as 100% (92/92) with two-sided 95% CI (95.99%, 100.00%), as shown in **Table 13**, below. For informational purposes, unadjusted PPA and NPA are also displayed.

Table 13. Concordance Analysis Comparing Sample-level Biomarker Detection between FoundationOne Liquid CDx and evNGS

		evNGS			
		<i>NTRK1/2/3</i> fusion positive	<i>NTRK1/2/3</i> fusion negative	Total	PPV/NPV (95% CI)
F1LCDx	<i>NTRK1/2/3</i> fusion positive ¹	4	6 ²	10	PPV: 40.0% (16.8%, 68.7%)
	<i>NTRK1/2/3</i> fusion negative	0	92	92	NPV: 100% (95.99%, 100%)
	Total	4	98	102	
	PPA/NPA (Unadjusted) (95% CI)	PPA: 100% (51.01%, 100%)	NPA: 93.9% (87.3%, 97.2%)		

¹No *NTRK2* fusion positive samples were evaluated in this study

²These six samples were discordant due to the fusion breakpoints falling in regions that the evNGS assay does not bait for.

The six (6) samples that were *NTRK1/2/3* fusion positive by FoundationOne Liquid CDx and *NTRK1/2/3* fusion negative by the evNGS were discordant due to the fusion breakpoints falling in regions that the evNGS assay does not bait for. Specifically, the evNGS assay did not claim to generate coverage in certain regions of interest (e.g., intron 8 of *NTRK1* and intron 5 of *ETV6*), and thus were negative by the evNGS comparator assay.

9.6 Concordance – FoundationOne Liquid CDx to an externally validated cfDNA NGS assay (EGFR exon 20 insertions)

An analytical accuracy study was performed to demonstrate the concordance between FoundationOne Liquid CDx and an externally validated cfDNA NGS comparator assay for the detection of *EGFR* exon 20 insertions. For this study, 101 frozen plasma samples were identified from patients enrolled in a clinical therapeutic study and 125 residual cfDNA samples were sourced from Foundation Medicine's clinical archives. Of the 125 residual cfDNA samples, four (4) were excluded due to diluted DNA concentration being out of acceptable range or evNGS post-sequencing QC failure. Of the 101 frozen plasma samples, 71 were excluded from the analysis due to insufficient cfDNA yield, diluted DNA concentration being out of acceptable range, or evNGS post-sequencing QC failure. Overall, a total of 151 samples from NSCLC patients were processed using both FoundationOne Liquid CDx and an externally validated cfDNA NGS assay in this study.

Analytical concordance was determined for the 151 samples that passed QC with both assays. Since specimens were selected based on FoundationOne Liquid CDx and confirmed by the evNGS assay, PPV and NPV are estimated conditional on FoundationOne Liquid CDx. Forty-nine (49) of the 151 samples were identified as positive for *EGFR* exon 20 insertions by both FoundationOne Liquid CDx and evNGS. The statistical analysis showed a PPV of 100% with two-sided 95% CI [92.70%-100%]

and a NPV of 99.02% with two-sided 95% CI [94.65%-99.83%], as shown in

Table 14 below.

Table 14. Concordance Analysis Comparing Sample-Level Biomarker Detection Between FoundationOne Liquid CDx and evNGS

		evNGS			
		<i>EGFR</i> exon 20 insertion positive	<i>EGFR</i> exon 20 insertion negative	Total	PPV/NPV (95% CI ¹)
F1LCDx	<i>EGFR</i> exon 20 insertion positive	49	0	49	PPV: 100% (92.70%, 100%)
	<i>EGFR</i> exon 20 insertion negative	1	101	102	NPV: 99.02% (94.65%, 99.83%)
	Total	50	101	151	
	PPA/NPA (Unadjusted) (95% CI ¹)	PPA: 98.00% (89.50%, 99.65%)	NPA: 100% (96.34%, 100%)		

In the one (1) discordant sample that was F1LCDx-negative/evNGS-positive, a 3 bp *EGFR* exon 20 insertion reported by the evNGS was not detected in the variant analysis pipeline of FoundationOne Liquid CDx.

9.7 Concordance – FoundationOne Liquid CDx to an externally validated ctDNA NGS assay (BRAF V600E)

An analytical accuracy study was performed to demonstrate the concordance between FoundationOne Liquid CDx and an externally validated ctDNA NGS (evNGS) comparator assay for the detection of *BRAF* V600E. Overall, a total of 304 samples from CRC (n=189) and NSCLC (n=115) patients were processed using both FoundationOne Liquid CDx and an externally validated ctDNA NGS assay in this study.

Analytical concordance using the evNGS assay results as the reference for the 304 samples that passed QC with both assays was determined. Since archived specimens were selected based on previous FoundationOne Liquid CDx or FoundationOne Liquid results and tested again by the evNGS assay and FoundationOne Liquid CDx, calculation of PPA and NPA is presented adjusted for the enrichment of *BRAF* V600E positives in the concordance evaluation sample cohort. Ninety-one (91) of the 304 samples were identified as positive for *BRAF* V600E by both FoundationOne Liquid CDx and the evNGS. Adjusted PPA has a point estimate of 98.91% with two-sided 95% CI [94.10%-99.81%]. Adjusted NPA has a point estimate of 100.00% with a 95% two-sided CI of [98.22%-100.00%]. For informational purposes, unadjusted PPA, NPA, PPV and NPV are also displayed, as shown in **Table 15**, below.

Table 15. Contingency Table Comparing the Detection of BRAF V600E by the FoundationOne Liquid CDx and Externally Validated ctDNA Assay

		evNGS			
		<i>BRAF</i> V600E positive	<i>BRAF</i> V600E negative	Total	PPV/NPV (Unadjusted) (95% CI)
F1LCDx	<i>BRAF</i> V600E positive	91	0	91	PPV: 100% (95.95%, 100%)
	<i>BRAF</i> V600E negative	1*	212	213	NPV: 9.53% (97.39%, 99.92%)
	Total	92	212	304	

	PPA/NPA (Unadjusted) (95% CI)	PPA: 98.91% (94.10%, 99.81%)	NPA: 100% (98.22%, 100%)		
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**This discordant sample had very low supporting reads and variant allele frequency in FoundationOne Liquid CDx, which did not pass FoundationOne Liquid CDx calling threshold.*

9.8 Concordance – FoundationOne Liquid CDx to an externally validated ctDNA NGS assay (HRR Gene Alterations)

An analytical accuracy study was performed to demonstrate the concordance between FoundationOne Liquid CDx and an externally validated ctDNA NGS (evNGS) comparator assay for the detection of nine (9) HRR genes (*ATR*, *CDK12*, *CHEK2*, *FANCA*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, and *RAD51C*). Overall, 163 samples (including 78 biomarker-negative and 85-biomarker positive as determined by F1LCDx results during the sample selection step and containing a total of 128 variants) from prostate cancer patients with valid results from both FoundationOne Liquid CDx and an externally validated ctDNA NGS assay were analyzed in this study. To align with the product specifications of the evNGS assay, variants below the threshold of 0.5% VAF as detected by the evNGS assay are excluded from analysis.

Sample-level analytical concordance was determined for the 163 samples that passed QC with both assays. The statistical analysis using the evNGS assay results as the reference showed a PPA of 97.26% with 95% CI [90.55%, 99.25%] and a negative percent agreement (NPA) of 82.22% with 95% CI [73.06%, 88.75%] unadjusted for prevalence (**Table 16**).

Table 16. Contingency Table Comparing the Sample-level Detection of HRR Gene Alterations by the F1LCDx Assay and the evNGS Assays

		evNGS Assay		
		Biomarker Positive	Biomarker Negative	Total
F1LCDx	Biomarker Positive	71	16	87
	Biomarker Negative	2	74	76
	Total	73	90	163

The concordance results at the variant-level are shown in Table 17. The statistical analysis using the evNGS assay results as the reference showed a PPA of 97.89% with 95% CI of [92.65%, 99.42%] and an NPA of 99.92% with 95% CI of [99.88%, 99.95%] as shown in **Table 17**

Table 17. Contingency Table Comparing the Variant-Level Detection of HRR Gene Alterations by the F1LCDx Assay and the evNGS Assays.

		evNGS Assay		
		Biomarker Positive	Biomarker Negative	Total
F1LCDx	Biomarker Positive	93	25	118
	Biomarker Negative	2	31,013	31,015
	Total	95	31,038	31,133

There were 27 discordant calls across 18 samples. Two variants detected by the evNGS assay but not

by F1LCDx were associated with low tumor fraction in the F1LCDx test. The remaining 25 alterations, detected by F1LCDx but not by the evNGS assay, included 15 variants in repetitive regions, 9 variants below the evNGS assay's LoD, and 1 complex deletion-insertion event potentially impacted by variant calling sensitivity.

9.9 Limit of Detection (Analytical Sensitivity)

The LoD for each variant type was established by processing a total of 1,069 sample replicates across ten contrived (enzymatically fragmented cell-line gDNA) samples representing short variants, rearrangements, and copy number alterations. The LoD was determined using the conservative hit rate approach for the majority of variants. A probit model was used when appropriate (when ≥ 3 dilution levels with hit rates between 10% and 90% were observed). LoD by hit rate was defined as the mean variant allele frequency (VAF) value (for short variants and rearrangements) or mean tumor fraction (TF) value (for copy number alterations) at the lowest dilution level tested with at least 95% detection across replicates. The hit rate was computed as the number of replicates with positive variant calls per the total number of replicates tested at each level of the targeted VAF (short variants and rearrangements) or tumor fraction (copy number alterations). Short variants with hit rates of at least 95% at all dilution levels or hit rates below 95% for all dilution levels were excluded from analysis as LoD could not be reliably estimated.

Confirmed LoDs for CDx alterations are presented below in **Table 18** and are taken from the confirmation of LoD studies as presented in Section 9.14. The confirmation of LoD studies utilized clinical samples assessed near the established LoD (targeting 1x-1.5x LoD). The confirmed LoD for targeted short variants, rearrangements, and copy number alterations demonstrate at least a 95% hit rate at a level near the established LoD (**Table 19**).

Table 18. Established and Confirmed LoD for CDx alterations

Tumor Type	Gene/variant	Alteration Subtype	Established LoD	Confirmed LoD (Fold LoD)
<i>Breast cancer</i>	<i>PIK3CA</i>	Substitutions	0.34% VAF	0.39% VAF (1.14x)
<i>CRC</i>	<i>BRAF</i> V600E	Substitution	0.33% VAF	0.70% VAF (2.12x)
	<i>BRCA1</i>	Copy Number Loss	Not Determined	61.80% TF (2.03x) ¹
<i>NSCLC</i>	<i>ALK</i>	Rearrangement	0.24% VAF	0.68% VAF (2.84x)
	<i>BRAF</i> V600E	Substitution	0.33% VAF	0.86% VAF (2.61x)
	<i>EGFR</i>	Substitutions (L858R)	0.34% VAF	0.64% VAF (1.90x)
		Indels (exon 19 deletions)	0.27% VAF	0.45% VAF (1.65x)
	<i>MET</i>	Substitutions (exon 14)	Not Determined	0.40% VAF (N/A) ¹
		Indels (exon 14)	0.41% VAF	0.28% VAF (0.67x)
	<i>ROS1</i>	Fusion	0.52% VAF	1.30% VAF (2.51x)
<i>Prostate cancer</i>	<i>ATM</i>	Substitutions	0.51% VAF	0.56% VAF (1.09x)
		Indels	0.51% VAF	0.86% VAF (1.68x)
		Rearrangement	Not Determined	1.13% VAF (N/A) ¹
	<i>ATR</i>	Rearrangements	Not Determined	0.52% VAF (1.42x) ¹
	<i>BRCA1</i>	Substitutions	0.34% VAF	0.51% VAF (1.49x)
		Indels	0.38% VAF	0.55% VAF (1.44x)
		Rearrangement	Not Determined	0.87% VAF (N/A) ^{1, 2}

Tumor Type	Gene/variant	Alteration Subtype	Established LoD	Confirmed LoD (Fold LoD)
	BRCA2	Substitutions	Not Determined	0.71% VAF (N/A) ¹
		Indels	0.36% VAF	0.63% VAF (1.74x)
		Rearrangement	Not Determined	0.48% VAF (N/A) ^{1, 3}
		Copy Number Loss	48.1% TF ⁴	N/A
	CDK12	Substitution	Not Determined	0.57% VAF (1.44x) ¹
	CDK12	Insertion	Not Determined	0.54% VAF (1.34x) ¹
	CDK12	Rearrangement	Not Determined	0.66% VAF (1.79x) ¹
	CHEK2	Deletion	Not Determined	0.57% VAF (1.43x) ¹
	CHEK2	Substitution	Not Determined	0.49% VAF (1.23x) ¹
	PALB2	Rearrangement	Not Determined	0.70% VAF (1.89x) ¹
	PALB2	Substitution	0.51% VAF	0.55% VAF (1.36x) ⁶
	FANCA	Rearrangement	Not Determined	1.21% VAF (1.35x) ¹
	FANCA	Insertion	Not Determined	1.40% VAF (1.70x) ¹
	MLH1	Deletion	Not Determined	1.25% VAF (1.53x) ¹
	MLH1	Rearrangement	Not Determined	1.16% VAF (1.29x) ¹
	MRE11A	Deletion	Not Determined	1.37% VAF (1.67x) ¹
	NBN	Substitution	Not Determined	1.30% VAF (1.59x) ¹
	RAD51C	Insertion	Not Determined	1.29% VAF (1.57x) ¹
	RAD51C	Rearrangement	Not Determined	1.22% VAF (1.35x) ¹
Solid tumors	NTRK1	Fusion	0.44% VAF	0.75% VAF (1.70x)
	NTRK3	Fusion	0.27% VAF	0.68% VAF (2.52x)

¹Confirmation of LoD was performed without direct LoD establishment data. Platform LoD was used for the targeted dilution level.

²Confirmed LoD for BRCA1 RE was using the DIBv1 primer set. LoD was also confirmed using the DIBv2 primer set at 1.27% VAF.

³Confirmed LoD for BRCA2 RE was using the DIBv1 primer set. LoD was also confirmed using the DIBv2 primer set at 1.49% VAF.

⁴LoD was established in a clinical sample and therefore confirmation of LoD was not applicable.

⁵ Fold LoD was calculated based on the platform LoD used for the targeted dilution level and not the established LoD.

The platform LoD for short variants, rearrangements, and copy number alterations are presented in **Table 19**. A total of 864 short variants were included in the platform LoD analysis. The enhanced sensitivity region of the bait set contains 269 of the short variants analyzed and the standard sensitivity region of the bait set contains 595 of the short variants analyzed. The estimated LoD for short variants is 0.40% for the enhanced sensitivity region and 0.82% of the standard sensitivity region. The median LoD is 30.4% tumor fraction for copy number losses.

Because a major component driving the detectability of a variant is genomic context (repetitiveness of the reference genomic region), the LoD analysis by alteration subtype was also evaluated within categories based on genomic context as summarized in **Table 19**.

Table 19. LoD by variant subtype based on genomic context

Region	Alteration Subtype	LoD Unit	N	Minimum LoD	1st Quantile LoD	Median LoD	3rd Quantile LoD
Enhanced Sensitivity Region	Short Variants: Enhanced Sensitivity Region Total	VAF	269	0.20%	0.33%	0.40%	0.50%
	Insertion/Deletion in non-repetitive region or a repetitive region of <=3 base pairs		10	0.23%	0.29%	0.31%	0.36%

Region	Alteration Subtype	LoD Unit	N	Minimum LoD	1st Quantile LoD	Median LoD	3rd Quantile LoD
	Insertion/Deletion in a repetitive region of 4 to 6 base pairs		23	0.28%	0.37%	0.48%	0.56%
	Insertion/Deletion in a repetitive region of >=7 base pairs		6	0.33%	0.48%	0.58%	0.82%
	Substitution in a non-repetitive region or a repetitive region of <=7 base pairs		229	0.20%	0.33%	0.39%	0.49%
	Substitution in a repetitive region of >7 base pairs		1	0.32%	0.32%	0.32%	0.32%
Standard Sensitivity Region	Short Variants: High Sensitivity Region Total	VAF	595	0.40%	0.70%	0.82%	0.98%
	Insertion/Deletion in non-repetitive region or a repetitive region of <=3 base pairs		18	0.46%	0.68%	0.87%	1.00%
	Insertion/Deletion in a repetitive region of 4 to 6 base pairs		32	0.61%	0.75%	0.87%	0.95%
	Insertion/Deletion in a repetitive region of >=7 base pairs		11	0.59%	1.07%	1.15%	1.20%
	Substitution in a non-repetitive region or a repetitive region of <=7 base pairs		524	0.40%	0.70%	0.81%	0.96%
	Substitution in a repetitive region of >7 base pairs		8	0.69%	0.83%	0.96%	1.28%
Enhanced Sensitivity Region	Rearrangements	VAF	7	0.20%	0.26%	0.37%	0.47%
Enhanced/Standard Sensitivity Region	Rearrangements	VAF	1	0.28%	0.28%	0.28%	0.28%
Standard Sensitivity Region	Rearrangements	VAF	1	0.90%	0.90%	0.90%	0.90%
NA	Copy Number Amplifications	TF	8	19.8%	19.8%	21.7%	25.2%
NA	Copy Number Losses	TF	2	12.70%	21.55%	30.40%	39.25%

The median LoD for highly-actionable, non-CDx alterations evaluated for LoD are presented in **Table 20**. The median LoD for these targeted short variants are consistent with the platform LoD presented in **Table 18**.

Table 20. LoD for non-CDx alterations

Gene	Alteration Subtype	Number of Samples Evaluated	Median LoD ¹
<i>BRAF</i>	Substitutions	1	0.33% VAF
<i>EGFR</i>	Indels	3	0.65% VAF
<i>ERBB2</i>	Copy Number Amplification	1	19.8% TF
<i>KRAS</i>	Substitutions	2	0.33% VAF
<i>MET</i> ²	Indels	1	0.41% VAF
<i>NRAS</i>	Substitutions	2	0.42% VAF
<i>PALB2</i>	Indels	1	0.37% VAF
	Substitutions	1	0.51% VAF

VAF = variant allele frequency TF = tumor fraction

¹Quantitative reporting of %VAF/%TF has not been approved by FDA.

²This LoD applies to *MET* alterations that do not meet the CDx rules.

9.10 Limit of Blank (LoB)

The study evaluated the limit of blank (LoB) of the F1LCDx assay updated with DIBv2 improvements. Two plasma cfDNA replicates and one replicate of donor-matched gDNA from 44 donors with no known cancer diagnosis, who were categorized in both age and smoking cohorts, were collected, extracted, and tested across 2 reagent lots where 2 cfDNA replicates and 1 matched gDNA replicate from each donor were tested in the same lot. A total of 87 cfDNA sample replicates (prepared from 44 donors x 2 replicates minus 1 replicate with DNA extraction failure) and 44 matched buffy coat gDNA sample replicates (single extraction from each of the 44 donors) were processed with F1LCDx across 2 reagent lots. Out of 132 sample replicates, 131 passed all QC specifications. LoB was assessed by calculating positive call rates for universal variants in technical blank samples simulated by excluding from F1LCDx cfDNA sample data variants identified in the matched donor gDNA F1LCDx data.

However, it should be noted that F1LCDx does not normalize patient samples with their germline DNA. Universal variants are defined as a set of variants detected at least once in any sample processed in F1LCDx validation studies. The LoB study results obtained in the technical blank samples are summarized in **Table 21** below.

Table 21. LoB Study Results in Technical Blanks

Variant Category	# of detected variants across all source samples (n=44) in a variant level	Total # of unique variants for a variant level in the universal set x Total # of source samples	False Positive Rate (%)	# of detected variants across all sample replicates (n=87) in a variant category	Per Sample Replicate False Positive Rate (%) [number of replicates with at least one detected variant/total sample replicates]
<u>Category 1:</u> ATM 1208C>G	1	39,512	0.0026	1	1.15% [1/87]
<u>Category 1:</u> BRCA 6116T>G	1	39,512	0.0026	1	1.15% [1/87]
<u>Category 1:</u> All other* CDx variants noted in Table 1 of Intended Use	0	39,512	0.0000	0	0.00% [0/87]
<u>Category 2:</u> cfDNA Biomarkers with Strong Evidence of Clinical Significance in cfDNA	0	44	0.0000	0	0.00% [0/87]
<u>Category 3:</u> Biomarkers with Evidence of Clinical Significance in tissue supported by: 3A: strong analytical validation using cfDNA 3B: analytical validation using cfDNA	2	13,288	0.0151	3	3.45% [3/87]
<u>Category 4:</u> Other Biomarkers with Potential Clinical Significance**	19	314,776	0.0060	22	19.54% [17/87]

*Note that the two false positives observed in Category 1, identified as ATM 2921+1G>C and BRAF 1799T>A, are excluded from the

false positive rate calculation of 'All other CDx variants' category.

****False positive results may be due to background signals inherent in sequencing methods designed for high sensitivity, clonal hematopoiesis of indeterminate potential, or germline polymorphisms.**

All CDx variants had false positive rate (FPR) < 5% and 2 CDx variants were detected at VAFs below the 0.40% VAF LoD for SNVs and indels in F1LCDx (a single call for *ATM*_1208C>G and a single call for *BRCA*_6116T>G, both at VAF around 0.10%).

Across all four categories reported by F1LCDx, FPR of on a per variant per sample replicate ranged from 1.15% (1 variant call out of 87 valid cfDNA replicates) to 2.30% (2 variant calls out of 87 valid sample replicates) for non-companion diagnostic variants (Categories 2-4 of the tumor profiling variants reported).

No rearrangements or copy number alterations were detected in any of the four categories.

Since a large number of non-CDx SNV and indel variants are detected in technical blanks at low VAF levels (less than 0.5% VAF for SNVs and 1% VAF for indels), i.e., in plasma from donors that do not have solid neoplasms after subtracting the presumably germline variants detected in the donors buffy coat, there is a risk that variants detected at very low allele frequency may be a false positive result. This risk may be due to background signals inherent in sequencing methods designed for high sensitivity. They may also be due to CHIP. Additional clinical investigation to confirm the presence of the variant in the patient's tumor with another FDA approved or cleared test is strongly recommended.

9.11 Potentially Interfering Substances

To evaluate the robustness of the FoundationOne Liquid CDx results in the presence of potentially interfering exogenous and endogenous substances, a total of 11 potential interferents were evaluated. These potential interferents included six endogenous substances (albumin, conjugated bilirubin, unconjugated bilirubin, cholesterol, hemoglobin and triglycerides) and five exogenous substances (DNA from another source [the microorganism *Staphylococcus epidermidis*], excess anticoagulant, proteinase K, ethanol and molecular index barcodes).

A total of 340 samples were tested to evaluate the potential interference of these substances. An assessment of the cfDNA yield obtained during the DNA isolation, purification, and quantification steps, as well as at library construction QC and hybrid capture QC was performed. The process success rates for each step are listed in **Table 22**.

Table 22. Process success rates with interfering substances

Process	# Failed	# Pass	Total	Success Rate (%)	95% CI LB (%)	95% CI UB (%)
DNA Extraction	0	180	180	100.00	97.97	100.00
LC	1	339	340	99.71	98.37	99.99
HC	3	336	339	99.12	97.44	99.82
Sequencing	0	336	336	100.00	98.91	100.00

For each potential interferent, concordance of alteration calls was calculated relative to a control sample without interferent. The pre-defined variants included 27 short variants, 17 rearrangements, and 3 copy number variants. Of the 11 potential interferents tested across 16 conditions, concordance for all variant calls was 100% for 8 conditions and ≥97% for all conditions (**Table 23**).

Table 23. Concordance per substance for variants $\geq 1\times$ LoD

Substance	Detected Reps	Total Reps	Concordance	95% two-sided exact CI_lower	95% two-sided exact CI_upper
Triglycerides, 37 mmol/L (or 33 g/L)	80	80	100.00%	95.49%	100.00%
Hemoglobin, 2.0 g/L	78	78	100.00%	95.38%	100.00%
Albumin, 60 g/L	80	82	97.56%	91.47%	99.7%
Bilirubin (conjugated), 0.2 g/L	84	84	100.00%	95.7%	100.00%
Bilirubin (unconjugated), 0.2 g/L	76	78	97.44%	91.04%	99.69%
Cholesterol Level 2, 3.88 mmol (150 mg/dL)	80	82	97.56%	91.47%	99.7%
Cholesterol Level 1, 6.47mmol (250 mg/dL)	74	76	97.37%	90.82%	99.68%
Staphylococcus epidermidis, 1 x 10 ⁶ CFU/mL	78	78	100.00%	95.38%	100.00%
Anticoagulant, 5X nominal volume	82	82	100.00%	95.6%	100.00%
Proteinase K, +0.6 mg/mL	98	99	98.99%	94.50%	99.97%
Proteinase K, +0.3 mg/mL	92	92	100.00%	96.07%	100.00%
Ethanol, +2.5%	96	98	97.96%	92.82%	99.75%
Ethanol, +5.0%	94	95	98.95%	94.27%	99.97%
Molecular Index barcodes, +5%	70	72	97.22%	90.32%	99.66%
Molecular Index barcodes, +15%	96	96	100.00%	96.23%	100.00%
Molecular Index barcodes, +30%	98	98	100.00%	96.31%	100.00%

Taken together, these data indicate that the FoundationOne Liquid CDx assay is robust to potential specimen- related endogenous substances and exogenous contaminants or interferents.

9.12 Hybrid Capture Bait Specificity

Bait specificity was addressed through an assessment of coverage of targeted regions in FoundationOne Liquid CDx using 3,546 validation study samples. Results show that targeted genomic regions have consistently high, uniform coverage. For each genomic region associated with a predefined subset of highly-actionable alterations, between 94% to 100% of samples possessed the expected level of coverage. An in-depth, platform-wide examination of the FoundationOne Liquid CDx baitset through the analysis of HapMap process control samples revealed that, on average, 98.8% and 94.1% of platform-wide baited coding and non-coding regions, respectively, met their expected coverage levels. Samples assessed in this study consistently demonstrated high quality uniform and deep coverage across the entire genomic region targeted by the assay.

9.13 Carryover/Cross-Contamination

The study demonstrated that the risk of cross contamination (intra-plate), and carry-over contamination (inter- plate) of samples during the processing of the FoundationOne Liquid CDx assay is low. A total of 376 wells were examined for intra-plate and inter-plate contamination by processing and sequencing of contrived samples derived from cell lines at high input concentrations with known genomic backgrounds. Unique variants of each cell line were characterized by independent control sequencing runs. The samples were arrayed in a checkerboard fashion across four 96-well PCR plates to detect cross-contamination events. A cross-contamination rate of 0.53% (2/376) was observed in this study. These data demonstrate a low probability of cross contamination during the FoundationOne Liquid CDx process.

9.14 Precision: Reproducibility and Confirmation of LoD

Multiple Precision and Confirmation of LoD studies were performed, using both clinical and contrived samples to evaluate precision and only clinical samples for confirmation of LoD. Precision was evaluated for alterations associated with both CDx claims and tumor profiling. Target alterations were assessed at two target levels each (near LoD and 2-3x LoD) for the contrived samples, and at one level (targeting 1-1.5x LoD) for clinical cfDNA samples.

In all studies, each sample was divided into 24 or 36 aliquots, with 2 replicates being processed on the same plate under the same conditions. Reproducibility was assessed and compared across three lots, two sequencers, and two processing runs for some studies, or across two lots, three sites, and three processing runs for certain studies (e.g., HRR genes). Samples were processed near the assay's minimum DNA input mass.

The studies evaluate the precision of FoundationOne Liquid CDx for detecting a set of highly actionable variants. **Table 24** and **Table 25** summarize the Disease Ontology (if applicable), Variant Subtype, Targeted Variant, Reproducibility, Observed Average Measurand, and LoD for each sample with CDx variants and non-CDx variants, respectively.

Table 24. Precision and Confirmation of LoD by Targeted CDx Variant

Targeted Variant	Variant Subtype	Cancer Type	Reproducibility (%) (95% Two-sided CI)	Observed Average Measurand	LoD
ALK_EML4_fusion	RE	Lung cancer	100 (86.2, 100)	0.68% VAF ¹	0.24% VAF
ALK-EML4 fusion	RE		100 (85.75, 100)	1.39% VAF ¹	0.24% VAF
ALK-EML4 fusion	RE	Contrived	100 (85.75, 100)	0.64% VAF	0.24% VAF
ALK-EML4 fusion	RE		100 (85.18, 100)	0.89% VAF	0.24% VAF
ALK-NPM1 fusion	RE		78.26 (56.3, 92.54)	0.4% VAF	0.94% VAF
ALK-NPM1 fusion	RE		100 (85.75, 100)	0.64% VAF	0.94% VAF
ATM K1773fs*3	Indel	Contrived	100 (85.75, 100)	0.77% VAF	0.51% VAF
ATM K1773fs*3	Indel		100 (85.18, 100)	1.04% VAF	0.51% VAF
ATM I2012fs*4	Indel	Prostate cancer	100 (85.18, 100)	0.86% VAF ¹	0.51% VAF
ATM splice site 8850+1G>A	Sub	Prostate cancer	100 (85.75, 100)	0.56% VAF ¹	0.51% VAF
ATM-EXPH5 truncation	RE		100 (85.75, 100)	1.13% VAF ¹	Not Determined
ATR-CMSS1	RE	Prostate cancer	94.44 (81.86, 98.46)	0.52% VAF	0.37% VAF ^{2,3}
ATR-2320delA	Indel		91.67 (78.17, 97.13)	0.08% VAF	0.40% VAF ^{2,3}
BRAF 1799T>A	Sub	CRC	100 (86.2, 100)	0.70% VAF ¹	0.33% VAF
BRAF 1799T>A	Sub	NSCLC	100 (85.13, 100)	0.86% VAF ¹	0.33% VAF
BRCA N1784fs*3	Indel	Stomach cancer	87.5 (69, 95.7)	0.34% VAF	0.36% VAF
BRCA1_loss	CN	CRC	100 (89.28, 100)	61.80% TF ¹	30.40% TF ^{2,3}
BRCA1 D825fs*21	Indel	Contrived	100 (85.75, 100)	0.61% VAF	0.38% VAF
BRCA1 D825fs*21	Indel		100 (85.75, 100)	0.93% VAF	0.38% VAF
BRCA1 P871fs*32	Indel		100 (85.18, 100)	0.51% VAF	0.38% VAF
BRCA1 P871fs*32	Indel		100 (85.75, 100)	1.08% VAF	0.38% VAF
BRCA1 Y465*	Sub	Prostate cancer	100 (86.2, 100)	0.51% VAF ¹	0.34% VAF
BRCA1_D1840fs*32	del		95.83 (79.76, 99.26)	0.55% VAF ¹	0.38% VAF
BRCA1_N/A_truncation	RE		100 (86.2, 100)	1.27% VAF ¹	Not Determined
BRCA2 C1200fs*1	Indel	Contrived	100 (85.75, 100)	0.58% VAF	0.36% VAF

Targeted Variant	Variant Subtype	Cancer Type	Reproducibility (%) (95% Two-sided CI)	Observed Average Measurand	LoD
BRCA2 C1200fs*1	Indel		100 (85.75, 100)	0.92% VAF	0.36% VAF
BRCA2 N1784fs*7	Indel		100 (85.75, 100)	1.22% VAF	0.36% VAF
BRCA2 N1784fs*7	Indel		100 (85.75, 100)	1.85% VAF	0.36% VAF
BRCA2 N1784fs*7	Indel		100 (85.18, 100)	1.07% VAF	0.36% VAF
BRCA2 N1784fs*7	Indel		100 (85.75, 100)	2.24% VAF	0.36% VAF
BRCA2 N1822fs*2	Indel		100 (85.75, 100)	0.92% VAF	0.36% VAF
BRCA2 N1822fs*2	Indel		100 (85.18, 100)	1.19% VAF	0.36% VAF
BRCA2 Q1429fs*9	Indel		100 (85.75, 100)	0.94% VAF	0.36% VAF
BRCA2 Q1429fs*9	Indel		100 (85.18, 100)	1.26% VAF	0.36% VAF
BRCA2 T3033fs*11	Indel		21.74 (7.46, 43.7)	0.71% VAF	0.36% VAF
BRCA2 T3033fs*11	Indel		91.67 (73, 98.97)	1.03% VAF	0.36% VAF
BRCA2_CDH17_truncation	RE	Prostate cancer	100 (86.2, 100)	1.49% VAF ¹	Not Determined
BRCA2_G995fs*4	del		95.83 (79.76, 99.26)	0.63% VAF ¹	0.36% VAF
BRCA2_loss	CN		100 (86.2, 100)	53.11% TF ¹	48.1% TF
BRCA2_loss	CN		87.5 (67.64, 97.34)	39.43% TF	48.1% TF
BRCA2_N/A_truncation	RE		70.83 (50.83, 85.09)	1.32% VAF	0.48% VAF
BRCA2_Q1361*	sub		100 (85.69, 100)	0.71% VAF ¹	0.49% VAF
BRCA2-EDA truncation	RE		100 (85.18, 100)	0.48% VAF ¹	0.47% VAF ²
CDK12_837C>G	Sub	Prostate cancer	100 (90.36, 100)	0.57% VAF ¹	0.40% VAF ^{2,3}
CDK12_2738_2739insA	Indel		100 (90.36, 100)	0.54% VAF ¹	0.40% VAF ^{2,3}
CDK12-MICALCL	RE		100 (90.11, 100)	0.66% VAF ¹	0.37% VAF ^{2,3}
CHEK2_1061T>A	Sub		94.44 (81.86, 98.46)	0.49% VAF	0.40% VAF ^{2,3}
CHEK2_1100delC	Indel		100 (90.36, 100)	0.57% VAF ¹	0.40% VAF ^{2,3}
EGFR E746_A750del	Indel	Lung cancer	95.7 (79, 99.2)	0.45% VAF ¹	0.27% VAF
EGFR E746_A750del	Indel		100 (84.56, 100)	0.34% VAF ¹	0.27% VAF
EGFR E746_A750del	Indel	Contrived	100 (85.75, 100)	0.51% VAF	0.27% VAF
EGFR E746_A750del	Indel		100 (85.75, 100)	0.74% VAF	0.27% VAF
EGFR E746_A750del	Indel		100 (85.75, 100)	0.93% VAF	0.27% VAF
EGFR E746_A750del	Indel		100 (85.18, 100)	1.2% VAF	0.27% VAF
EGFR E746_A750del	Indel		100 (85.18, 100)	0.51% VAF	0.27% VAF
EGFR E746_A750del	Indel		100 (85.75, 100)	1.01% VAF	0.27% VAF
EGFR E746_A750del	Indel		100 (85.75, 100)	1.01% VAF	0.27% VAF
EGFR L858R	Sub	Lung cancer	100 (85.75, 100)	0.64% VAF ¹	0.34% VAF
EGFR L858R	Sub		100 (85.75, 100)	1.64% VAF ¹	0.34% VAF
EGFR L858R	Sub	Contrived	100 (85.75, 100)	0.46% VAF	0.34% VAF
EGFR L858R	Sub		100 (85.75, 100)	0.68% VAF	0.34% VAF
EGFR L858R	Sub		100 (85.75, 100)	0.68% VAF	0.34% VAF
EGFR L858R	Sub		100 (85.18, 100)	0.95% VAF	0.34% VAF
ETV6-NTRK3 fusion	RE	Thyroid cancer	100 (86.20, 100)	0.82% VAF ¹	0.27% VAF
ETV6-NTRK3 fusion	RE	Contrived	95.83 (78.88, 99.89)	0.32% VAF	0.474% VAF ²
ETV6-NTRK3 fusion	RE		95.83 (78.88, 99.89)	0.59% VAF	0.474% VAF ²
ETV6-NTRK3 fusion	RE	Lung cancer	100 (85.75, 100)	26.33% VAF	0.474% VAF ²

Targeted Variant	Variant Subtype	Cancer Type	Reproducibility (%) (95% Two-sided CI)	Observed Average Measurand	LoD
ETV6-NTRK3 fusion	RE	Salivary gland cancer	100 (85.69, 100)	0.68% VAF ¹	0.27% VAF
FANCA-N/A	RE	Prostate cancer	97.14 (85.47, 99.49)	1.21% VAF ¹	0.90% VAF ^{2,3}
FANCA_1290G>AT	Indel		100 (90.36, 100)	1.40% VAF ¹	0.82% VAF ^{2,3}
GOPC-ROS1 fusion	RE	Contrived	86.96 (66.41, 97.22)	0.35% VAF	0.474% VAF ²
GOPC-ROS1 fusion	RE		91.67 (73, 98.97)	0.91% VAF	0.474% VAF ²
MET exon14 splice site 2888-35 2889>A	Indel	Lung cancer	95.8 (79.8, 99.3)	0.28% VAF ¹	0.41% VAF
MET exon14 splice site 3028+1G>T	Sub		95.8 (79.8, 99.3)	0.45% VAF ¹	Not Determined
MET exon14 splice site 3028+2T>C	Sub		95.7 (79.0, 99.2)	0.35% VAF ¹	Not Determined
MET exon14splice site 3028+1G>T	Sub		100 (85.7, 100)	0.85% VAF	Not Determined
MET exon14splice site 3028+2T>C	Sub		100 (85.75, 100)	0.76% VAF	Not Determined
MET splice site 3029-1G>T	Sub	Contrived	62.5 (40.59, 81.2)	0.21% VAF	Not Determined
MET splice site 3029-1G>T	Sub		91.3 (71.96, 98.93)	0.3% VAF	Not Determined
MET splice site 2888-17 2888-3del15	Indel	Lung cancer	100 (85.75, 100)	1.17% VAF ¹	0.41% VAF
MET splice site 3005_3028+3>C	Indel		100 (85.75, 100)	1.67% VAF ¹	0.41% VAF
MLH1_1851delG	Indel	Prostate cancer	100 (90.36, 100)	1.25% VAF ¹	0.82% VAF ^{2,3}
MLH1-TMPRSS2	RE		100 (90.36, 100)	1.16% VAF ¹	0.90% VAF ^{2,3}
MPRIIP-NTRK1 fusion	RE	Contrived	69.57 (47.08, 86.79)	0.49% VAF	0.44% VAF
MPRIIP-NTRK1 fusion	RE		87.5 (67.64, 97.34)	0.69% VAF	0.44% VAF
MRE11A-1543-1546delGAAG	Indel	Prostate cancer	100 (90.36, 100)	1.37% VAF ¹	0.82% VAF ^{2,3}
MRE11A-N/A	RE		80.56 (64.97, 90.25)	1.05% VAF	0.90% VAF ^{2,3}
PALB2-N/A	RE		100 (90.11, 100)	0.70% VAF ¹	0.37% VAF ^{2,3}
PALB2_49-1G>C	Sub		96.88 (84.26, 99.45)	0.55% VAF ¹	0.51% VAF ³
NBN_2152G>T	Sub		100 (90.11, 100)	1.30% VAF ¹	0.82% VAF ^{2,3}
NBN-N/A	RE		86.11(71.34, 93.92)	1.16% VAF	0.90% VAF ^{2,3}
PIK3CA E542K	Sub	Breast cancer	100 (85.75, 100)	0.89% VAF ¹	0.34% VAF
PIK3CA E545A	Sub	Contrived	100 (85.75, 100)	0.52% VAF	0.34% VAF
PIK3CA E545A	Sub		100 (85.18, 100)	0.7% VAF	0.34% VAF
PIK3CA E545K	Sub		100 (85.75, 100)	0.45% VAF	0.34% VAF
PIK3CA E545K	Sub		100 (85.75, 100)	0.66% VAF	0.34% VAF
PIK3CA H1047R	Sub	Breast cancer	100 (85.75, 100)	1.04% VAF ¹	0.34% VAF
PIK3CA H1047R	Sub	Contrived	100 (85.18, 100)	0.41% VAF	0.34% VAF
PIK3CA H1047R	Sub		100 (85.75, 100)	0.76% VAF	0.34% VAF
PIK3CA Q546R	Sub	Breast cancer	91.7 (74.2, 97.7)	0.44% VAF	0.34% VAF
PIK3CA Q546R	Sub	Contrived	95.65 (78.05, 99.89)	0.49% VAF	0.34% VAF
PIK3CA Q546R	Sub		100 (85.75, 100)	0.92% VAF	0.34% VAF
PIK3CA_H1047R	Sub	Breast cancer	95.65 (79.01, 99.23)	0.39% VAF ¹	0.34% VAF
RAD51C_444_445insT	Indel	Prostate cancer	100 (90.36, 100)	1.29% VAF ¹	0.82% VAF ^{2,3}
RAD51C-N/A	RE		94.44 (81.86, 98.46)	1.22% VAF	0.90% VAF ^{2,3}

Targeted Variant	Variant Subtype	Cancer Type	Reproducibility (%) (95% Two-sided CI)	Observed Average Measurand	LoD
ROS1-CD74 fusion	RE	Lung cancer	100 (85.75, 100)	1.32% VAF ¹	0.52% VAF
ROS1-EZR fusion	RE		100 (85.75, 100)	1.3% VAF ¹	0.52% VAF
SLC34A2-ROS1 fusion	RE	Contrived	100 (85.75, 100)	1.03% VAF	0.284% VAF ²
SLC34A2-ROS1 fusion	RE		100 (85.18, 100)	1.36% VAF	0.284% VAF ²
TPM3-NTRK1 fusion	RE	Lung cancer	91.67 (73, 98.97)	8.48% VAF	0.44% VAF
TPM3-NTRK1 fusion	RE	Contrived	100 (85.75, 100)	0.3% VAF	0.44% VAF
TPM3-NTRK1 fusion	RE		100 (85.75, 100)	0.4% VAF	0.44% VAF
TPM3-NTRK1 fusion	RE	Colon cancer	100 (85.69, 100)	0.83% VAF ¹	0.44% VAF
TPR-NTRK1 fusion	RE	Thyroid cancer	100 (85.69, 100)	0.75% VAF ¹	0.44% VAF

¹LoD was confirmed for these variants with hit rate (same as the reproducibility) which met the acceptance criteria defined in respective study.

² LoD was not determined for these specific variants; platform LoD for the variant type is listed.

³Results were obtained from samples tested with 36 replicates across 3 sites

Table 25. Precision and Confirmation of LoD by Targeted Non-CDx Variant

Targeted Variant	Variant Subtype	Cancer Type	Reproducibility (%) (95% Two-sided CI)	Observed Average Measurand	LoD
BRAF L597R	Sub	Contrived	95.65 (78.05, 99.89)	0.42% VAF	0.49% VAF
BRAF L597R	Sub		100 (85.75, 100)	0.85% VAF	0.49% VAF
BRAF V600E	Sub	Skin cancer	100 (85.75, 100)	0.44% VAF ¹	0.33% VAF
BRAF V600E	Sub	Contrived	100 (85.18, 100)	0.72% VAF	0.49% VAF
BRAF V600E	Sub		100 (85.75, 100)	1.38% VAF	0.49% VAF
BRAF V600K	Indel	Skin cancer	95.83 (78.88, 99.89)	0.36% VAF ¹	0.33% VAF
BRCA1 E23fs*17	Indel	Ovarian cancer	100 (85.75, 100)	0.66% VAF ¹	0.38% VAF
BRCA1 Q780*	Sub		100 (85.75, 100)	1.11% VAF ¹	0.34% VAF
BRCA1_S646fs*5	del		100 (85.69, 100)	0.54% VAF ¹	0.38% VAF
BRCA1_Y1563*	Sub		100 (86.2, 100)	1.66% VAF ¹	0.51% VAF
BRCA1-BRCA1 deletion	RE		100 (85.75, 100)	0.87% VAF ¹	0.28% VAF ²
BRCA2 G267*	Sub		91.67 (73, 98.97)	0.5% VAF	Not Determined
BRCA2 S2988fs*12	Indel		100 (85.75, 100)	1.07% VAF ¹	0.36% VAF
BRCA2_E2198fs*4	del		100 (86.2, 100)	0.65% VAF ¹	0.36% VAF
BRCA2_N3124I	Sub		100 (86.2, 100)	0.74% VAF ¹	0.49% VAF
BRCA2 R2842C	Sub	Lung cancer	100 (85.7, 100)	0.57% VAF ¹	0.49% VAF
EGFR S492R	Sub	Colon cancer	71.4 (45.4, 88.3)	0.39% VAF	0.34% VAF
EGFR T790M	Sub	Lung cancer	100 (85.75, 100)	1.26% VAF ¹	0.34% VAF
EGFR T790M	Sub	Contrived	100 (85.18, 100)	0.36% VAF	0.49% VAF
EGFR T790M	Sub		100 (85.75, 100)	0.65% VAF	0.49% VAF
EGFR T790M	Sub		100 (85.75, 100)	0.44% VAF	0.49% VAF
EGFR T790M	Sub		100 (85.75, 100)	0.66% VAF	0.49% VAF
EGFR ex20 insertion H773_V774insH	Indel	Lung Cancer	100 (86.2, 100)	0.98% VAF ¹	Not Determined
EGFR ex20 insertion V769_D770insASV	Indel		100 (86.2, 100)	1.28% VAF ¹	Not Determined
EGFR ex20 insertion D770_N771insSVD	Indel		100 (86.2, 100)	0.65% VAF ¹	Not Determined
ERBB2_amplification	CN	Breast cancer	100 (85.75, 100)	61.73% TF ¹	19.8% TF
ERBB2_amplification	CN	Lung cancer	100 (85.69, 100)	0% TF ¹	19.8% TF
ERBB2_amplification	CN	Colon cancer	100 (86.2, 100)	31.05% TF ¹	19.8% TF

Targeted Variant	Variant Subtype	Cancer Type	Reproducibility (%) (95% Two-sided CI)	Observed Average Measurand	LoD
ERBB2_amplification	CN	Unknown primary cancer	100 (85.69, 100)	33.12% TF ¹	19.8% TF
ERBB2_amplification	CN	Contrived	100 (85.75, 100)	35.78% TF	25.2% TF
ERBB2_amplification	CN		100 (85.75, 100)	39.79% TF	25.2% TF
ERBB2_amplification	CN	Soft tissue cancer	0 (0, 13.8)	54.53% TF	19.8% TF
ERBB2_amplification	CN	Lung cancer	0 (0, 14.31)	54.8% TF	19.8% TF
KRAS G12D	Sub	Contrived	100 (85.75, 100)	0.89% VAF	0.49% VAF
KRAS G12D	Sub		100 (85.18, 100)	1.12% VAF	0.49% VAF
KRAS G12L	Sub	Colon cancer	100 (85.75, 100)	0.49% VAF ¹	0.33% VAF
KRAS G13D	Sub	Contrived	100 (85.75, 100)	0.55% VAF	0.49% VAF
KRAS G13D	Sub		100 (85.75, 100)	0.82% VAF	0.49% VAF
KRAS G13D	Sub		100 (85.18, 100)	0.57% VAF	0.49% VAF
KRAS G13D	Sub		100 (85.75, 100)	0.92% VAF	0.49% VAF
KRAS G13D	Sub		100 (85.75, 100)	0.92% VAF	0.49% VAF
KRAS Q61R	Sub	Colon cancer	100 (85.75, 100)	0.53% VAF ¹	0.33% VAF
MET L1312fs*4	Indel	Contrived	100 (85.75, 100)	0.69% VAF	0.56% VAF
MET L1312fs*4	Indel		100 (85.75, 100)	0.96% VAF	0.56% VAF
NRAS G12C	Sub		100 (85.75, 100)	0.69% VAF	0.49% VAF
NRAS G12C	Sub		100 (85.75, 100)	0.96% VAF	0.49% VAF
NRAS G12C	Sub	Lung cancer	91.3 (73.2, 97.6)	0.55% VAF	0.42% VAF
NRAS G12D	Sub	Contrived	82.61 (61.22, 95.05)	0.48% VAF	0.49% VAF
NRAS G12D	Sub		100 (85.75, 100)	0.84% VAF	0.49% VAF
NTRK2-N/A rearrangement	RE		95.83 (78.88, 99.89)	1.85% VAF	0.897% VAF
NTRK2-N/A rearrangement	RE		95.83 (78.88, 99.89)	2.03% VAF	0.897% VAF
PALB2 G808*	Sub		100 (85.18, 100)	0.47% VAF	0.49% VAF
PALB2 G808*	Sub		100 (85.75, 100)	0.92% VAF	0.49% VAF
PALB2 K908fs*15	Indel		100 (85.75, 100)	0.52% VAF	0.56% VAF
PALB2 K908fs*15	Indel		100 (85.75, 100)	0.74% VAF	0.56% VAF
PALB2 N280fs*8	Indel	Colon cancer	100 (56.6, 100)	0.48% VAF ¹	0.37% VAF
PIK3CA D549N	Sub	Contrived	100 (85.75, 100)	0.48% VAF	0.49% VAF
PIK3CA D549N	Sub		100 (85.75, 100)	0.73% VAF	0.49% VAF

¹ LoD was confirmed for these variants with hit rate (same as the reproducibility) which met the acceptance criteria defined in respective study.

² LoD was not determined for these specific variants; platform LoD for the variant type is listed.

Assessment of Tumor Profiling Variants

Across 39 unique samples, including 8 contrived samples, and 31 clinical samples, a total of 1,240 variants were evaluated for reproducibility and repeatability of tumor profiling variants, with variant types including substitutions, indels, rearrangements, and copy number alterations. The number of variants in each variant bin are summarized in **Table 26**. The overall reproducibility results were 99.59% with the 95% 2-sided exact CIs [99.58%, 99.60%]. The overall repeatability for all variants were 99.47% with 95% 2-sided exact CIs [99.45%, 99.48%]. The reproducibility and repeatability results for each variant type are summarized in **Table 26**.

Table 26. Number of each variant type

Variant Category	N	# of Pairs Agree/ # of Total Pairs	Repeatability (%) [95% Two-Sided Exact CIs (%)]	# of Replicates Agree/ # of Total Replicates	Reproducibility (%) [95% Two-Sided Exact CIs (%)]
Substitutions	898				
Substitution in a non-repetitive region or a repetitive region of <=7 base pairs	882				
Substitution in a repetitive region of >7 base pairs	16				
Indels	228	126475 / 127224	99.41 [99.37, 99.45]	254509 / 255588	99.58 [99.55, 99.60]
Insertion/Deletion in non-repetitive region or a repetitive region of <=3 base pairs	52				
Insertion/Deletion in a repetitive region of 4 to 6 base pairs	118				
Insertion/Deletion in a repetitive region of >=7 base pairs	58				
Rearrangements	60	33105 / 33480	98.88 [98.76, 98.99]	66723 / 67260	99.20 [99.13, 99.27]
Copy Number Alterations	54	29880 / 30132	99.16 [99.05, 99.26]	60115 / 60534	99.31 [99.24, 99.7]
Copy Number Amplification	49				
Copy Number Loss	5				
Total	1240	688225 / 691920	99.47 [99.45, 99.48]	1384328 / 1390040	99.59 [99.58, 99.60]

9.15 Reagent Lot Interchangeability

The interchangeability of critical reagent lots for library construction (LC), hybrid capture (HC) and sequencing within the FoundationOne Liquid CDx assay was evaluated by testing eight (8) contrived samples from either enzymatically fragmented cell line genomic DNA containing alterations of interest or enzymatically fragmented plasmid DNA. Each of the contrived samples was tested in triplicate using two different lots each of LC, HC, and sequencing reagents. Eight reagent pairings were assessed. A total of eight analyses for each specimen were completed. A total of 192 tests were included in this study. Four Master Pool Libraries (MPLs) were evaluated on each of two flowcells on a NovaSeq 6000 sequencer, using two different sequencing reagent lots. Of the 49 alterations assessed in the sample set, 43 had a percent agreement greater than 90% (39 alterations had percentage agreement equal to 100%, one had percent agreement equal to 95.83%, one had percent agreement equal to 95.65%, and two had percent agreement equal to 91.67%), exceeding the pre-specified acceptance criteria. For the remaining six alterations the observed detection rates for these variants were similar to the predicted detection rate based on the LoD analysis. These results demonstrate the interchangeability of critical reagent lots in the FoundationOne Liquid CDx assay.

9.16 Variant Curator Precision

This study was performed to evaluate the precision of genomic variant call curation, following analysis by the FoundationOne Liquid CDx analysis pipeline. This was established by analyzing targeted alterations, including CDx alterations, and platform-wide alterations within samples used in the FoundationOne Liquid CDx Precision and LoD and Precision Confirmation Study. The study design reflected the intermediate precision design and evaluated curator precision in reporting of targeted and

platform alterations. A total of 19 samples were selected for this study. Three curators were chosen randomly amongst all qualified curators to curate variant calls in a set of randomly chosen replicates from each of the 19 samples. The variant calls were generated from each sample per curator. The overall average percent agreement for targeted alterations was 93.3% (95% CI; 83.80%, 98.15%), and for platform genomic alterations was 99.14% (95% CI; 98.47%, 99.57%).

9.17 Stability

9.17.1 Reagent Stability

The reagent stability of FoundationOne Liquid CDx was assessed by analyzing data from each of eight samples in triplicate, per each of three different lots of LC, HC, and sequencing reagents. A total of nine analyses for each specimen were completed for each of six time points assessed. A total of 72 tests were assessed per time period; a total of 432 samples and six time points (one baseline timepoint and 5 subsequent experimental timepoints) were included in this study overall. Each of the three sample Master Library Pools (MPLs), representing three LC and HC reagent lots was evaluated per time point on a NovaSeq 6000 sequencer, using three different sequencing reagent lots. The analysis of baseline timepoint zero (T0) identified the baseline variant calls for each sample.

All five experimental time points have been processed and analyzed for Lot #1, Lot #2, and Lot #3. Concordance was assessed among 127,642 data points for tumor profiling variants across the five experimental timepoints. The three reagent lots achieved $\geq 90\%$ concordance with the baseline variant calls for all the experimental timepoints (including the last two timepoints T4 and T5 at 12 and 13 months respectively) except for a middle timepoint T3 (9 months) which is present in **Table 27**. The reason for the failure of T3 (9 months) was a technical error which resulted in lower than planned DNA being transferred for LC and therefore this was not a reagent failure. Reagent stability can be claimed as 12 months.

Table 27. Concordance for Tumor Profiling Variants at Replicate Level by Reagent Lot and by Timepoint

Reagent Lot	Timepoint ¹	# Concordant	# Total	Concordance (%)	95% 2-sided score CI (%)
LOT#1	3 months	1921	1966	97.71%	[96.95%, 98.28%]
	6 months	2082	2151	96.79%	[95.96%, 97.46%]
	9 months	1916	2151	89.07%	[87.69%, 90.32%]
	12 months	1609	1656	97.16%	[96.25%, 97.86%]
	13 months	1918	1973	97.21%	[96.39%, 97.85%]
LOT#2	3 months	2083	2148	96.97%	[96.16%, 97.62%]
	6 months	2091	2160	96.81%	[95.98%, 97.47%]
	9 months	1851	2160	85.69%	[84.15%, 87.11%]
	12 months	2087	2160	96.62%	[95.77%, 97.3%]
	13 months	2089	2160	96.71%	[95.87%, 97.39%]
LOT#3	3 months	2086	2139	97.52%	[96.77%, 98.10%]
	6 months	2098	2154	97.4%	[96.64%, 97.99%]
	9 months	1855	2154	86.12%	[84.59%, 87.51%]
	12 months	2097	2154	97.35%	[96.59%, 97.95%]
	13 months	1924	1977	97.32%	[96.51%, 97.94%]

A supplemental study is being conducted to evaluate the stability of updated LC reagents. The study will confirm that reagent stability can be claimed as 12 months for the FoundationOne Liquid CDx assay with the changed reagents.

9.17.2 Whole Blood Specimen Stability

The recommended storage temperature is 18°C - 25°C. In this study, stress conditions were simulated through extended storage at elevated (35°C ± 2°C) and reduced (4° ± 2°C) temperatures. In this interim analysis, 22 samples (11 sample pairs) were tested, including baseline (within 24 hours of collection) and experimental time points (after 10, 14, or 15 days of storage).

Overall, 100% of samples yielded a cfDNA input ≥30ng. The success rate for DNAX yield, and LC yield was 100% and the success rate of the HC yield was 96.3%. The variant analysis was conducted for variants at ≥2x LoD. For the aggregate 11 pairs of samples processed and reported, 100% agreement was observed between the baseline and experimental timepoint for short variants and rearrangements for each experimental time point. The percent agreement per sample also resulted in 100% agreement between the baseline and experimental timepoint for short variants and rearrangements. The data is summarized in **Table 28**.

Table 28. Aggregate percent agreement per temperature and experimental timepoint

Temperature	Experimental Timepoint	N	Short Variants [95% two-sided CI]	Rearrangements
4°C	7 Days	4	100.00 [89.72, 100.00]	100.00 [39.76, 100.00]
	14 Days	3	100.00 [91.40, 100.00]	N/A
	15 Days	3	100.00 [83.89, 100.00]	N/A
35°C	14 Days	1	N/A	N/A

The impact of potential interferents originating from the FoundationOne Liquid cfDNA blood collection tube (BCT) stopper on the performance of the FoundationOne Liquid CDx assay was assessed by evaluating stability of whole blood in tubes stored in an upright or inverted position at 4°C± 2°C, 25°C± 2°C, and 35°C± 2°C for various durations (10, 14, and 15 days).

First, the success rate of the FoundationOne Liquid CDx assay for processing samples was assessed at the DNA extraction (DNAX), LC, HC, and sequencing steps based on product in-process QC criteria. Samples stratified by the upright and the inverted condition exhibited comparable success rates above 94% at DNAX, LC, HC, and sequencing (**Table 29**). Thus, the stopper of the FoundationOne Liquid cfDNA BCT does not impact FoundationOne Liquid CDx test performance when stored between 4°C - 35°C for up to 15 days.

Table 29. Process success rate by tube position

Process	Tube Position	# Passing Samples	# Total Samples	Success Rate (%)	95% 2-sided CIs (%)
DNA Extraction	Upright	139	147	94.6%	[89.6%, 97.2%]
	Inverted	147	150	98%	[94.3%, 99.3%]
LC	Upright	135	136	99.3%	[96%, 99.9%]
	Inverted	146	146	100%	[97.4%, 100%]
HC	Upright	134	135	99.3%	[95.9%, 99.9%]
	Inverted	143	146	97.9%	[94.1%, 99.3%]
Sequencing	Upright	134	134	100%	[97.2%, 100%]
	Inverted	143	143	100%	[97.4%, 100%]

Stability was also evaluated by comparing concordance between baseline and experimental samples. PPA and NPA for alteration calls at ≥ 2x LoD were computed along with the corresponding two-sided 95% score confidence interval (CI) across all replicates by variant category using the baseline detection as reference. Note that NPA is under-estimated as variants not detected at any of the treatment

conditions were not used in the analysis set and hence counted against the NPA calculation.

Concordance between baseline and experimental results from all samples in the upright and inverted position combined demonstrated >99% PPA and NPA for the detection of short variants and rearrangements. Copy number alterations were only detected in samples treated in the inverted tube position and therefore, not included in this analysis. Furthermore, stratification by the treatment condition (2 tube positions × 3 temperatures × 3 durations) revealed >99.0% PPA and NPA for short variants and rearrangements across the combinations of tube positions, temperatures and durations tested. The data also demonstrate that the detection of copy number alterations is not impacted by the storage of blood in the inverted position at 35°C for up to 14 days. The concordance results by variant type for each of the experimental conditions are provided in **Table 30**.

Table 30. Concordance of detected alterations between baseline sample and experimental conditions for inverted tube stability study

Variant Type	Temp.	Tube Position	Exp. Time Point	N Variants Detected at Baseline Time Point	N Variants Detected at Exp. Time Point	N Variants Agree	PPA	PPA [95% CI]	N Variants Not Detected at Baseline Time Point	N Variants Not Detected at Exp. Time Point	NPA	NPA [95% CI]
Short variants	04°C	Inverted	Day 10	50	50	49	98%	[89.5%, 99.6%]	612	612	100%	[100%, 100%]
Short variants	04°C	Upright	Day 10	50	51	50	100%	[92.9%, 100%]	613	612	100%	[100%, 100%]
Short variants	04°C	Inverted	Day 14	59	58	58	98.3%	[90.9%, 99.7%]	610	611	100%	[100%, 100%]
Short variants	04°C	Upright	Day 14	44	44	44	100%	[92.0%, 100%]	611	611	100%	[100%, 100%]
Short variants	04°C	Inverted	Day 15	37	37	37	100%	[90.6%, 100%]	611	611	100%	[100%, 100%]
Short variants	04°C	Upright	Day 15	52	52	52	100%	[93%, 100%]	611	611	100%	[100%, 100%]
Short variants	25°C	Inverted	Day 10	78	77	76	97.1%	[91.1%, 99.2%]	627	628	100%	[100%, 100%]
Short variants	25°C	Upright	Day 10	44	44	44	100%	[92.0%, 100%]	613	613	100%	[100%, 100%]
Short variants	25°C	Inverted	Day 14	46	48	46	100%	[92.3%, 100%]	611	609	100%	[100%, 100%]
Short variants	25°C	Upright	Day 14	42	41	41	97.6%	[87.7%, 99.6%]	610	611	100%	[100%, 100%]
Short variants	25°C	Inverted	Day 15	44	44	44	100%	[92.0%, 100%]	613	613	100%	[100%, 100%]
Short variants	25°C	Upright	Day 15	49	48	48	97.8%	[89.3%, 99.6%]	616	617	100%	[100%, 100%]
Short variants	35°C	Inverted	Day 10	15	15	15	100%	[79.6%, 100%]	609	609	100%	[100%, 100%]
Short variants	35°C	Upright	Day 10	35	35	35	100%	[90.1%, 100%]	609	609	100%	[100%, 100%]
Short variants	35°C	Inverted	Day 14	55	55	55	100%	[93.4%, 100%]	611	611	100%	[100%, 100%]
Short variants	35°C	Upright	Day 14	48	47	46	95.7%	[86.0%, 98.8%]	609	610	100%	[100%, 100%]
Short variants	35°C	Inverted	Day 15	39	39	38	97.4%	[86.8%, 99.5%]	610	610	100%	[100%, 100%]
Short variants	35°C	Upright	Day 15	28	29	28	100%	[87.9%, 100%]	613	612	100%	[100%, 100%]

These results demonstrate that blood is stable in the FoundationOne Liquid CDx cfDNA BCT when stored between 4°C - 35°C for up to 15 days, in an upright or inverted position. Additional data will be

generated to further evaluate whole blood stability and potential interference of the blood collection tube cap.

9.18 DNA Extraction

DNA extraction evaluated 72 samples across five cancer types: lung cancer (including NSCLC), CRC, prostate cancer, breast cancer, and skin cancer (melanoma, sarcoma) using three reagent lots and two KingFisher Magnetic Particle processors.

Reproducibility of the FoundationOne Liquid CDx DNA extraction process across KingFisher instruments and extraction reagent lots were analyzed utilizing a factorial design (3 reagent lots × 2 KingFisher instruments × 2 replicates). The success rate of the DNAX yield for three reagent lots range from 95.8% to 100.0% and two King Fisher instruments range from 97.2% to 100.0%.

Variant calls included in the concordance analysis were identified based on the majority call across all 12 replicates for a given disease ontology. PPA and NPA were computed across the replicates for each somatic alteration for each sample, and aggregated by variant type (deletion, insertion, rearrangement, and substitution) for variants at ≥1x LoD. The percent agreement results by disease ontologies are: 90.3% - 99.8 % for PPA, and 99.1% - 100.0% for NPA (**Table 31**) The percent agreement results across all variant types (deletion, insertion, rearrangement and substitution) evaluated at ≥1x LoD are: 90.6%-96.8% for PPA and 98.9% - 100.0% for NPA (**Table 32**).

Table 31. Concordance summary by disease ontology at 1x LoD for DNA extraction study

Disease Ontology	Positive Detected/ Positive Total	PPA [95% two-sided CI]	Negative Detected/ Negative Total ¹	NPA [95% two-sided CI]	Overall Detected/ Total*	OPA [95% two-sided CI]
Breast Cancer	347/348	99.7% [98.4%,100.0%]	3144/3144	100.0% [99.9%,100.0%]	3491/3492	100.0% [99.8%,100.0%]
CRC	1122/1188	94.4% [93.0%,95.7%]	2284/2304	99.1% [98.7%,99.5%]	3406/3492	97.5% [97.0%,98.0%]
Lung Cancer	431/432	99.8% [98.7%,100.0%]	3053/3060	99.8% [99.5%,99.9%]	3484/3492	99.8% [99.5%,99.9%]
NSCLC	600/612	98.0% [96.6%,99.0%]	2878/2880	99.9% [99.7%,100.0%]	3478/3492	99.6% [99.3%,99.8%]
Prostate Cancer	486/492	98.8% [97.4%,99.6%]	2987/3000	99.6% [99.3%,99.8%]	3473/3492	99.5% [99.2%,99.7%]
Skin Cancer	455/504	90.3% [87.4%,92.7%]	2987/2988	100.0% [99.8%,100.0%]	3442/3492	98.6% [98.1%,98.9%]

¹Variants detected include variants classified as VUS and benign

Table 32. Concordance summary by variant type at 1x LoD for DNA extraction study

Variant Type	Positive Detected/ Positive Total	PPA [95% two-sided CI]	Negative Detected/ Negative Total ¹	NPA [95% two- sided CI]	Overall Detected/ Total*	OPA [95% two- sided CI]
Deletions	386/ 408	94.6% [91.9%, 96.6%]	2036/ 2040	99.8% [99.5%, 99.9%]	2422/ 2448	98.9% [98.4%, 99.3%]
Insertions	163/ 180	90.6% [85.3%, 94.4%]	819/ 828	98.9% [97.9%, 99.5%]	982/ 1008	97.4% [96.2%, 98.3%]
Rearrangements	23/ 24	95.8% [78.9%, 99.9%]	120/ 120	100.0% [97.0%, 100.0%]	143/ 144	99.3% [96.2%, 100.0%]
Substitutions	2869/ 2964	96.8% [96.1%, 97.4%]	14358/ 14388	99.8% [99.7%, 99.9%]	17227/ 17352	99.3% [99.1%, 99.4%]

¹Variants detected include variants classified as VUS and benign

These results demonstrate robustness of the FoundationOne Liquid CDx DNA extraction process across KingFisher instruments, extraction reagent lots, and cancer types.

9.19 Guard Banding/Robustness

This validation study evaluated the impact on FoundationOne Liquid CDx test performance due to potential process variation with regard to uncertainty in the measurement of DNA concentration. This guard banding evaluation assessed the DNA input into each of the main process steps of the FoundationOne Liquid CDx assay (LC, HC, and sequencing).

Guard bands were evaluated relative to calculated process variability for LC, HC, and sequencing. The assessment of multiple DNA input levels into LC demonstrated robust performance and tolerance of various DNA input levels. The observed results of HC guard banding showed that the HC process is robust within the predefined specifications 1000ng to 2000ng of DNA input into HC. For sequencing, the observed distribution of coverage indicated robust performance within the predefined specifications of 1.0nM of DNA input concentration into sequencing (as summarized in **Table 33**).

Table 33. Summary of process pass and failure rate at each guard banding DNA input level

Process ¹	Input Level		# of Pass	Pass Rate (%)
HC	-50%	500ng	18/20	90
	-20%	800ng	20/20	100
	Lower limit	1000ng	20/20	100
	Upper limit	2000ng	20/20	100
	+20%	2400ng	20/20	100
	+50%	3000ng	18/20	90
Sequencing	-50%	0.5nM	20/20	100
	-20%	0.8nM	20/20	100
	Normal input	1.0nM	20/20	100
	+20%	1.2nM	20/20	100
	+50%	1.5nM	20/20	100

¹ Results for guardbanding of LC input levels can be found in **Table 32** below.

A second guard banding study was conducted to evaluate the impact of a range of cfDNA input masses (50% below the lower limit and 33% above the upper limit) for FoundationOne Liquid CDx using an updated LC input range (20-60ng). Results from this second study are described in **Table 34** and **Table 35**. All 105 sample replicates tested in this study passed processing and post-sequencing metric specifications as shown in **Table 34** below. The results demonstrate robust performance across the intended DNA input range.

Table 34. Processing Success Rates by cfDNA Input Level for FoundationOne Liquid CDx

Process QC	cfDNA Input Level	cfDNA Input (ng)	# Total	# Pass	# Fail	Success Rate	95% Two-sided Score CI
LC	-50%	10	21	21	0	100%	[84.54%, 100%]
	Lower limit	20	21	21	0	100%	[84.54%, 100%]
	Mid-point	40	21	21	0	100%	[84.54%, 100%]
	Upper limit	60	21	21	0	100%	[84.54%, 100%]
	+33%	80	21	21	0	100%	[84.54%, 100%]
HC	-50%	10	21	21	0	100%	[84.54%, 100%]
	Lower limit	20	21	21	0	100%	[84.54%, 100%]

Process QC	cfDNA Input Level	cfDNA Input (ng)	# Total	# Pass	# Fail	Success Rate	95% Two-sided Score CI
	Mid-point	40	21	21	0	100%	[84.54%, 100%]
	Upper limit	60	21	21	0	100%	[84.54%, 100%]
	+33%	80	21	21	0	100%	[84.54%, 100%]
Sequencing	-50%	10	21	21	0	100%	[84.54%, 100%]
	Lower limit	20	21	21	0	100%	[84.54%, 100%]
	Mid-point	40	21	21	0	100%	[84.54%, 100%]
	Upper limit	60	21	21	0	100%	[84.54%, 100%]
	+33%	80	21	21	0	100%	[84.54%, 100%]
Post-sequencing QC	-50%	10	21	21	0	100%	[84.54%, 100%]
	Lower limit	20	21	21	0	100%	[84.54%, 100%]
	Mid-point	40	21	21	0	100%	[84.54%, 100%]
	Upper limit	60	21	21	0	100%	[84.54%, 100%]
	+33%	80	21	21	0	100%	[84.54%, 100%]

Table 35. Aggregate Percent Agreement Across All Targeted Variants per cfDNA Input Level for FoundationOne Liquid CDx

cfDNA Input Level	cfDNA Input (ng)	Agreement (# Variants Detected / Total # Variants) [95% Two-sided Score CI]
-50%	10	92.86% (117/126) [86.98%, 96.2%]
Lower limit	20	99.21% (125/126) [95.64%, 99.86%]
Mid-point	40	100% (126/126) [97.04%, 100%]
Upper limit	60	100% (126/126) [97.04%, 100%]
+33%	80	100% (126/126) [97.04%, 100%]

9.20 Pan-Tumor Performance

A large-scale retrospective analysis was performed to demonstrate consistent test performance of FoundationOne Liquid CDx across samples derived from patients with different tumor types. This was evaluated by comparing in-process QC metrics across tumor types using historical data from samples processed in Foundation Medicine's clinical laboratory using two prior versions of the FoundationOne Liquid CDx assay. The FoundationOne Liquid CDx assay was developed based on two versions of the FoundationOne Liquid Laboratory Developed Test (LDT) assay, each of which targeted a subset of the genomic regions targeted by FoundationOne Liquid CDx. FoundationACT (FACT) targeted 62 genes and FoundationOne Liquid targeted 70 genes. The workflow is substantially similar between the assays. In order to support the use of historical data in this study, the regions commonly baited by the two previous assay versions and by FoundationOne Liquid CDx were evaluated for comparability of test performance (Section 2.15). The sample set for this analysis included 19,868 distinct samples from 25 tumor type categories that had previously been tested using the Foundation Medicine FoundationOne Liquid and FoundationACT assays, previous versions of FoundationOne Liquid CDx. **Table 36** below includes a summary of the tissue types included in the study. Overall, 98.1% of samples yielded ≥ 25 ng DNA, which corresponds to a DNA input mass of 20ng for LC. A total of 89.1% of samples yielded ≥ 36 ng of DNA which corresponds to a DNA input mass of 30ng for LC. The proportion of samples with an LC yield greater than the minimum mass of 500ng and lower than the maximum mass of 27000ng was 99.9%, with one sided 95% confidence interval of [99.8%, 99.9%]. The proportion of samples with an HC yield greater than the minimum mass of 20ng and lower than the maximum mass of 2250ng was 100%, with one sided 95% confidence interval of [99.99%, 100%]. The proportion of samples which met coverage requirements was 96.1%, with one sided 95% confidence interval of

[95.9%, 96.3%]. The proportion of samples which met post-sequencing requirements was 95.6%, with one sided 95% confidence interval of [95.3%, 95.8%]. The proportion of samples that generated a passing or qualified (overall pass as results are reported) result after sequencing was 91.7%, with one-sided 95% confidence interval of [91.4%, 92.1%].

Table 36. FoundationOne Liquid/FACT samples per tumor type and pass rates

Tumor Type	Sample Size	DNA Extraction Pass Rate (≥25 ng ²)	DNA Extraction Pass Rate (≥36 ng ¹)	LC Yield Pass Rate	HC Yield Pass Rate	Median Coverage Pass Rate	Post-sequencing Pass Rate	Overall Pass Rate (≥36 ng ¹)	Overall Pass Rate (≥25 ng ²)
Biliary Cancer	171	99.4%	95.3%	100.0%	100.0%	98.8%	97%	97.5%	95.9%
Bladder Cancer	166	97.6%	85.5%	100.0%	100.0%	93.2%	98.7%	95.8%	92%
Breast Cancer	2775	97.6%	87.7%	99.9%	100.0%	96.4%	95.5%	95.8%	91.9%
Cholangio-carcinoma	377	98.9%	96.0%	99.7%	100.0%	98.7%	97.3%	97%	95.7%
Colorectal Cancer (CRC)	1640	98.5%	92.4%	99.9%	100.0%	97.5%	96.9%	96.1%	94.3%
Endocrine-Neuro Cancer	75	100.0%	85.3%	100.0%	100.0%	100.0%	93.3%	96.9%	93.3%
Endometrial Cancer	231	98.3%	88.3%	100.0%	100.0%	96.5%	95.9%	95.1%	92.5%
Esophagus Cancer	291	99.7%	92.4%	100.0%	100.0%	97.6%	96.5%	96.3%	94.1%
Glioma Cancer	59	94.9%	72.9%	100.0%	100.0%	100.0%	76.8%	86%	76.8%
Head and Neck Cancer	154	96.1%	81.8%	100.0%	100.0%	89.2%	96.2%	95.2%	85.8%
Kidney Cancer	203	99.0%	87.7%	100.0%	100.0%	95.0%	95.3%	94.9%	90.5%
Liver Cancer	109	98.2%	95.4%	100.0%	100.0%	100.0%	95.3%	95.2%	95.3%
Lung Non-Small Cell Lung Carcinoma (NSCLC)	5919	98.2%	88.8%	99.8%	100.0%	95.5%	95.6%	94.7%	91.1%
Melanoma	257	96.5%	79.8%	100.0%	100.0%	92.7%	93.5%	93.7%	86.7%
Ovary Cancer	496	97.8%	88.5%	100.0%	100.0%	95.9%	94.6%	94.5%	90.7%
Pancreas Cancer	1359	98.8%	94.0%	99.9%	100.0%	97.8%	95.8%	95%	93.6%
Peripheral Nervous System (PNS)	44	100.0%	90.9%	100.0%	100.0%	100.0%	93.2%	95%	93.2%
Prostate Cancer	1778	97.3%	87.7%	99.9%	100.0%	96.9%	95.1%	95.8%	92.1%
Rare Tumors	1164	97.0%	86.4%	99.9%	100.0%	93.8%	94.3%	93.4%	88.4%
Small Cell Cancer	135	98.5%	93.3%	100.0%	100.0%	99.2%	99.2%	98.4%	98.5%
Soft Tissue Sarcoma	130	97.7%	83.1%	100.0%	100.0%	95.3%	91.7%	94.4%	87.4%
Stomach Cancer	267	98.9%	89.1%	100.0%	100.0%	98.1%	93.8%	95.8%	92%
Thyroid Cancer	50	98.0%	86.0%	100.0%	100.0%	100.0%	81.6%	90.7%	81.6%
Unspecified	856	98.5%	89.1%	100.0%	100.0%	95.5%	96.6%	96.3%	92.3%
Unknown Primary Carcinoma (CUP)	1162	98.1%	89.7%	100.0%	100.0%	95.2%	95.9%	94.8%	91.3%

¹ 36 ng of extracted cfDNA allows for sufficient cfDNA to process 30 ng of cfDNA

² 25 ng of extracted cfDNA allows for sufficient cfDNA to process 20 ng of cfDNA

Table 37 summarizes the overall sample pass rate across tumor types as well as performance metrics from key QC points in the process. These results demonstrate comparable test performance across tumor types.

Table 37. Summary of FoundationOne Liquid/FACT sample data

QC Metric	QC Pass Rate Across Tumor Types ¹	Tumor Types with ≥ 90% QC Pass Rate
Overall report Pass/Qualified rate	76.8%~98.5%	24/25 (96%) ²
Library Construction	99.7%~100%	25/25 (100%) ¹
Hybridization Capture	100%	25/25 (100%) ¹
Median exon coverage	89.2%~100%	24/25 (96%) ¹
Post-sequencing	76.8%~99.2%	23/25 (92%) ¹

¹ Summarized based on 25ng of Extracted cfDNA

² Summarized based on 36ng of Extracted cfDNA

9.21 Concordance – FoundationOne Liquid LDT to FoundationOne Liquid CDx

In order to support the use of historical data from the FoundationOne Liquid LDT to evaluate performance across cancer types, a study was performed to evaluate concordance between FoundationOne Liquid CDx and the FoundationOne Liquid LDT across the genomic regions targeted by both assays. This study evaluated the concordance of 927 unique samples processed on both the FoundationOne Liquid LDT and FoundationOne Liquid CDx assays. A total of 3,366 alterations, consisting of only those in common between the assays were evaluated. The concordance analysis using FoundationOne Liquid LDT or FoundationOne Liquid CDx as the reference assay is summarized by variant category in **Table 38**.

Table 38. Concordance between FoundationOne Liquid LDT (F1L LDT) and FoundationOne Liquid CDx

Variant/ Mutation Type	F1LCDx+ F1L LDT+	F1LCDx- F1L LDT+	F1LCDx+ F1L LDT-	F1LCDx- F1L LDT -	PPA [95% CI]	NPA [95% CI]	OPA [95% CI]
All Short Variants	2871	123	32	1171180	95.9% [95.1%-96.6%]	>99.9% [>99.9%-100.0%]	>99.9% [>99.9%-100.0%]
Base Substitutions	2415	104	31	999032	95.9% [95.0%-96.6%]	>99.9% [>99.9%-100.0%]	>99.9% [>99.9%-100.0%]
Indels	456	19	1	172148	96.0% [93.8%-97.6%]	>99.9% [>99.9%-100.0%]	>99.9% [>99.9%-100.0%]
Rearrangements	147	20	24	59587	88.0% [82.1%-92.5%]	>99.9% [>99.9%-100.0%]	99.9% [99.9%-99.9%]
Copy Number Amplifications	173	32	0	59463	84.4% [78.7%-89.1%]	99.8% [>99.9%-100.0%]	99.8% [>99.9%-100.0%]
Total	3191	175	166	1290230	94.8% [94.0%-95.5%]	>99.9% [>99.9%-100.0%]	>99.9% [>99.9%-100.0%]

The overall PPA between FoundationOne Liquid LDT and FoundationOne Liquid CDx assays, with FoundationOne Liquid LDT as the reference assay, was 94.8% with a 95% two-sided CI of [94.0%-95.5%]. The respective short variant, rearrangement, and copy number amplification PPA values, with 95% two-sided CI, were: 95.9% [95.1%-96.6%], 88.0% [82.1%-92.5%], and 84.4% [78.7%-89.1%].

These results support the agreement between FoundationOne Liquid LDT and FoundationOne Liquid CDx and the applicability of the tumor comparability analysis performed using historical FoundationOne Liquid data.

9.22 Molecular Index Barcode Performance

To evaluate the molecular index barcode performance, a total of 7,641 sequenced samples from FoundationOne Liquid CDx validation studies were analyzed with the FoundationOne Liquid CDx assay.

The overall coefficient of variation (% CV) of sequencing coverage across all barcodes was 8.95% for the enhanced sensitivity regions and 7.64% for the standard sensitivity regions. This observed small % CV includes both sample variability and barcode variability as these two components were confounded and inseparable. Results demonstrated that all 480 barcodes analyzed are detectable with low differences in sample coverage variance between barcodes, indicating comparable performance of the barcodes.

9.23 Automation Line Equivalence

An intermediate precision study was performed to establish equivalence between the Hamilton instrumentation and the Biomek/Bravo instrumentation. The study consisted of eight contrived samples run in triplicate across four runs and both instrumentation platforms resulting in a total of 192 sample replicates included in the study overall. The analysis evaluated the negative call rate (NCR) and positive call rate (PCR) for 1,309 variants from eight contrived samples. The PCR and NCR were also evaluated by the seven variant categories.

The Mann-Whitney test was used for the comparison of PCR and NCR across liquid handling platforms for each sample, all samples in aggregate, and for each variant type. The NCR across platforms for each analysis set (per sample, all samples in aggregate, per variant type) were not statistically significant ($p > 0.05$). by sample and by variant type. The PCR across platforms were not statistically significant ($p > 0.05$) with the exception of contrived sample #3, the aggregate of all samples, and substitutions in a non-repetitive region or a repetitive region of ≤ 7 base pairs. The PCRs for the Hamilton liquid handling platform were slightly higher than the PCRs for the Biomek/Bravo platform (92.08% versus 90.15% for sample #3, 90.75% versus 89.67% for all samples, and 91.14% versus 90.10% for substitutions in a non-repetitive region or repetitive region of ≤ 7 base pairs). The statistical significance observed was due to large sample sizes allowing for the detection of slight differences that are likely not meaningful in practice; therefore, the Hamilton and Biomek/Bravo liquid handling platforms are considered to be interchangeable in the FoundationOne Liquid CDx assay.

9.24 Updated LC Method Comparison Study

A method comparison study was conducted to demonstrate comparable performance between FoundationOne Liquid CDx assay using original and updated LC input ranges. Eighty-one clinical cfDNA samples from 10 unique disease ontologies were processed in triplicate to create 243 sample replicates. Samples were processed at the lower range for cfDNA input, 30ng for the original recommended minimum for LC input and 20ng for the updated minimum for LC input. 1,815 unique targeted variants were analyzed including CDx variants and variants from all alteration sub-types.

For each of the 81 samples, two of the three replicates were processed with FoundationOne Liquid CDx around a 30ng input level, using the previous LC method, (referred to as CCD₁ and CCD₂) and the third replicate was processed with FoundationOne Liquid CDx around a 20ng input level, using the updated LC method, (referred to as UCD_{ALL}). The 243 sample replicates tested in this study passed all QC metrics. A non-inferiority analysis was performed. Aggregated PPA and NPA across all 1,815 targeted variants were calculated for pairwise comparisons between CCD₁ and CCD₂. PPAs and NPAs for all targeted variants were also calculated for either CCD₁ or CCD₂ versus UCD_{ALL}. Agreement differences were calculated with corresponding 95% upper 1-sided bounds. The upper bounds of the 1-sided 95% CIs for agreement differences ζ_{PPA1} , ζ_{PPA2} , ζ_{NPA1} and ζ_{NPA2} were all $< 1\%$ for UCD_{ALL}. Therefore, the FoundationOne Liquid CDx assay using the updated LC input range was demonstrated to be non-

inferior to FoundationOne Liquid CDx using the original LC input range for the detection of CDx and non-CDx variants.

9.25 Updated F1LCDx LC and HC Processes

Analytical validation studies were performed to support the updated LC and HC workflow to the F1LCDx assay. Two of the studies performed (Method Comparison and Limit of Blank) are detailed below in **Sections 9.25.1 and 9.25.2**

9.25.1 Method Comparison Study

This study evaluated the LC and HC workflow updates to the F1LCDx assay compared to the originally approved F1LCDx test configuration. Seventy-eight (78) unique cfDNA specimens from a wide variety of tumor types were tested in this study using a non-inferiority (NI) study design. Three replicates of each of these 78 cfDNA specimens were prepared (234 sample replicates in total): CCD₁ and CCD₂ (two replicates; representing the original test configuration), and UCD (one replicate; representing the updated test configuration with LC/HC improvements). In total, 229 out of 234 CCD/UCD replicates were sequenced successfully for an overall success rate of 97.86%.

For the primary NI analysis, a total of 437 unique targeted variants (including both targeted CDx and targeted non-CDx variants) were analyzed. Targeted variants are defined as variants reported when detected by F1LCDx that have a result $\geq 1\times$ LoD in either CCD₁ or CCD₂. Non-targeted variants are any other variants detected and reported by F1LCDx, either by CCD₁ or CCD₂, including variants with levels below 1x LoD for which the sample was not selected.

Aggregated PPAs and NPAs across all targeted variants were estimated for the pair-wise comparisons between CCD₁ and CCD₂, and between UCD and CCD with CCD₁ or CCD₂ as reference and calculated separately. The results of aggregated agreements and differences between aggregated agreements (ζ_{PPA1} , ζ_{PPA2} , ζ_{NPA1} , ζ_{NPA2}) with corresponding 95% upper 1-sided confidence interval (CI) bounds are provided in **Table 39**.

Table 39. Non-Inferiority Testing of the Aggregated Agreement Results for Targeted Variants

NI Statistics	CCD ₁ & CCD ₂ Agreement (%)	UCD & CCD Agreement (%)	Agreement Difference ζ (%)	Upper bound of 95% one-sided CI for ζ^1 (%)
$\zeta_{PPA1} = (PPA_{C1C2} - PPA_{C1U})$	96.77	96.58	0.19	1.38
$\zeta_{PPA2} = (PPA_{C2C1} - PPA_{C2U})$	95.86	97.36	-1.51	-0.08
$\zeta_{NPA1} = (NPA_{C1C2} - NPA_{C1U})$	99.93	99.93	0.00	0.03
$\zeta_{NPA2} = (NPA_{C2C1} - NPA_{C2U})$	99.95	99.96	-0.01	0.02

¹CIs for agreement differences were calculated based on Newcombe 1988 method for paired data

The upper bounds of the 1-sided 95% CIs for agreement differences ζ_{PPA1} , ζ_{PPA2} , ζ_{NPA1} and ζ_{NPA2} were all $<1.5\%$. Aggregated PPAs and NPAs across all tumor profiling variants (includes targeted and non-targeted variants) were also estimated for the pair-wise comparisons between CCD₁ and CCD₂, and between UCD and CCD with CCD₁ or CCD₂ as reference and calculated separately. The results of aggregated agreements and differences between aggregated agreements (ζ_{PPA1} , ζ_{PPA2} , ζ_{NPA1} , ζ_{NPA2}) with corresponding 95% upper 1-sided confidence interval (CI) bounds are provided in **Table 40**.

Table 40. Non-Inferiority Testing of the Aggregated Agreement Results for Reportable Tumor Profiling Variants

NI Statistics	CCD ₁ & CCD ₂ Agreement (%)	UCD & CCD Agreement (%)	Agreement Difference ζ (%)	Upper bound of 95% one-sided CI for ζ^1 (%)
$\zeta_{PPA1} = (PPA_{C1C2} - PPA_{C1U})$	88.41	88.12	0.29	2.11
$\zeta_{PPA2} = (PPA_{C2C1} - PPA_{C2U})$	81.77	86.60	-4.83	-2.70
$\zeta_{NPA1} = (NPA_{C1C2} - NPA_{C1U})$	99.71	99.85	-0.14	-0.11
$\zeta_{NPA2} = (NPA_{C2C1} - NPA_{C2U})$	99.83	99.93	-0.10	-0.08

The upper bounds of the 1-sided 95% CIs for agreement differences ζ_{PPA1} , ζ_{PPA2} , ζ_{NPA1} and ζ_{NPA2} were all <2.11%. Concordance analyses were performed for tumor profiling variants by short variant type, i.e., substitutions, insertions, and deletion (**Table 41**). The discordances observed are due to low level VAF ($\leq 1\%$), however the level of concordance is comparable between CCD1 and CCD2, and between UCD and CCD1 and CCD2 indicating that the updated F1LCDx assay is non-inferior for calling tumor profiling substitutions, insertions, and deletion variants.

Table 41. Aggregated Agreement Results for Reportable Tumor Profiling Short Variants by Variant Subtype

Aggregated Agreement	Point Estimate (%) (Numerator/Denominator) [Two-sided 95% Score CI (%)]		
	Substitution	Insertion	Deletion
$\alpha\alpha PPA_{C1C2}$	89.87 (275/306) [85.98, 92.77]	78.26 (54/69) [67.18, 86.36]	87.57 (162/185) [82.04, 91.57]
$\alpha\alpha NPA_{C1C2}$	99.74 (23868/23930) [99.67, 99.80]	99.78 (5030/5041) [99.61, 99.88]	99.62 (14506/14561) [99.51, 99.71]
$\alpha\alpha PPA_{C1U}$	90.85 (278/306) [87.09, 93.59]	72.46 (50/69) [60.95, 81.61]	88.11 (163/185) [82.65, 92.01]
$\alpha\alpha NPA_{C1U}$	99.85 (23894/23930) [99.79, 99.89]	99.86 (5034/5041) [99.71, 99.93]	99.82 (14535/14561) [99.74, 99.88]
$\alpha\alpha PPA_{C2C1}$	81.60 (275/337) [77.12, 85.38]	83.08 (54/65) [72.18, 90.28]	74.65 (162/217) [68.47, 79.98]
$\alpha\alpha NPA_{C2C1}$	99.87 (23868/23899) [99.82, 99.91]	99.70 (5030/5045) [99.51, 99.82]	99.84 (14506/14529) [99.76, 99.89]
$\alpha\alpha PPA_{C2U}$	88.61 (319/360) [84.91, 91.49]	82.35 (56/68) [71.64, 89.61]	81.17 (181/223) [75.52, 85.75]
$\alpha\alpha NPA_{C2U}$	99.93 (25518/25536) [99.89, 99.96]	99.94 (5389/5392) [99.84, 99.98]	99.92 (15520/15533) [99.86, 99.95]

To demonstrate that the updated F1LCDx is non-inferior to the originally approved F1LCDx for copy

number alterations reported by the test as listed in **Table 1** and **Table 3** above, 2 samples with *BRCA2* homozygous deletions, and 7 samples positive for *ERBB2* amplifications, including 4 samples with copy number amplification near the threshold for positivity were tested. All 9 samples were concordant among all replicates tested (UCD and CCD₁ and CCD₂), indicating that the updated F1LCDx assay is non-inferior for calling copy number alterations approved for the device.

To demonstrate that the updated F1LCDx is non-inferior to the originally approved F1LCDx for rearrangements and fusions reported by the test as listed in Table 1 and 3, 1 sample with a *ROS1* fusion, and 5 samples positive for *NTRK1/2/3* fusions/rearrangements, 4 samples positive for *ALK* fusions/rearrangements, 4 samples with *ATM* rearrangements and 5 samples with *BRCA1/2* rearrangements were evaluated. All *ROS1* fusion and *NTRK1/2/3* fusion/rearrangement samples with valid results were concordant among all replicates tested (UCD and CCD₁ and CCD₂). Among the 4 *ALK* fusion/rearrangements samples tested, only 1 was concordant among CCD₁ and CCD₂, however the variant was not detected in the UCD replicate. All four samples had low fusion read levels near threshold required for positivity. Similarly for *ATM* and *BRCA1/2* rearrangements of the 9 samples positive for these alterations, only 3 samples (1 *ATM* and 2 *BRCA2* rearrangements) were concordant across all three replicate (UCD and CCD₁ and CCD₂), while the remaining were discordant among UCD and CCD₁ and CCD₂ to a similar extent. The reason for the discordance were attributed low read support.

9.25.2 Limit of Blank Study

The study evaluated the LoB of the updated F1LCDx assay using LC and HC improvements. Two plasma cfDNA replicates and one replicate of donor-matched gDNA from 47 donors with no known cancer diagnosis, who were categorized in both age and smoking status cohorts, were collected, extracted, and tested, with 24 out of the 47 donors tested with one reagent lot, and the remaining 23 donors tested with another reagent lot. Of the 94 cfDNA replicates and the paired 47 gDNA replicates, all replicates passed QC specifications.

Therefore, all 47 donors and their matched gDNA and cfDNA replicates were used in the statistical analysis. False positive rates (FPRs) were computed with variants in the universal set in technical blank replicates for each Category reported by F1LCDx and on a per sample replicate basis. Technical blanks replicate results represent variant results obtained after removing variants detected in a patient's buffy coat which are likely to represent germline variants. However, it should be noted that F1LCDx does not normalize patient samples with their germline DNA. The universal set U consists of all unique variants detected in previous F1LCDx validation studies up until January 2022, and all variants detected in this LoB study. The LoB study results obtained in the technical blank samples are summarized in **Table 42** below.

Table 42. LoB Study Results in Technical Blanks

Variant Category	# of detected variants across all source samples (n=47) in a variant level	Total # of unique variants for a variant level in the universal set × Total # of source samples	False Positive Rate (%)	# of detected variants across all sample replicates (n=94) in a variant category	Per Sample Replicate False Positive Rate (%) [number of replicates with at least one detected variant/total sample replicates]
Category 1: ATM 2921+1G>C	1	42,488	0.0024	2	2.13% [2/94]

<u>Category 1:</u> <i>BRAF</i> 1799T>A	1	42,488	0.0024	1	1.06% [1/94]
<u>Category 1:</u> All other* CDx variants noted in Table 1 of Intended Use	0	42,488	0.0000	0	0.00% [0/94]
<u>Category 2:</u> cfDNA Biomarkers with Strong Evidence of Clinical Significance in cfDNA	0	47	0.0000	0	0.00% [0/94]
<u>Category 3:</u> Biomarkers with Evidence of Clinical Significance in tissue supported by: 3A: strong analytical validation using cfDNA 3B: analytical validation using cfDNA	1	14,335	0.0070	1	1.06% [1/94]
<u>Category 4:</u> Other Biomarkers with Potential Clinical Significance**	24	338,353	0.0071	31	30.85% [29/94]

*Note that the two false positives observed in Category 1, identified as *ATM* 2921+1G>C and *BRAF* 1799T>A, are excluded from the false positive rate calculation of 'All other CDx variants' category.

**False positive results may be due to background signals inherent in sequencing methods designed for high sensitivity, clonal hematopoiesis of indeterminate potential, or germline polymorphisms.

All CDx variants had false positive rate (FPR) < 5% and 2 CDx variants were detected at VAFs below the 0.40% VAF LoD for SNVs and indels in F1LCDx (2 calls for *ATM*_2921+1G>C in paired replicates from the same donor: VAF = 0.12% and 0.13%; a single call for *BRAF*_1799T>A: VAF = 0.10%). Across all four categories reported by F1LCDx, FPR of on a per variant per sample replicate ranged from 1.06% (1 variant call out of 94 valid cfDNA replicates) to 2.13% (2 variant calls out of 94 valid sample replicates) for non-companion diagnostic variants (Categories 2-4 of the tumor profiling variants reported). No rearrangements or copy number alterations were detected in any of the four categories.

Since a large number of non-CDx SNV and indel variants are detected in technical blanks at low VAF levels (less than 0.5% VAF for SNVs and 1% VAF for indels), i.e., in plasma from donors that do not have solid neoplasms after subtracting the presumably germline variants detected in the donors buffy coat, there is a risk that variants detected at very low allele frequency may be a false positive result. This risk of false positivity identified based on the LoB study results in the updated F1LCDx is the same as the risk identified for originally approved F1LCDx, refer to **Section 9.10**. This risk may be due to background signals inherent in sequencing methods designed for high sensitivity. They may also be due to CHIP. Additional clinical investigation to confirm the presence of the variant in the patient's tumor with another FDA approved or cleared test is strongly recommended.

9.25.3 HC Yield Pass Rate

Confirmation of HC yield pass rate utilized samples and replicates from two LC/HC validation studies (Method Comparison and Limit of Blank). Given a total of 172 samples/replicates across the 2 studies, 172 samples/replicates passed HC yield specification (≥ 38.5 ng and < 600 ng), with an overall HC yield pass rate of 100%, which passed the acceptance criteria of 90%. These results demonstrate that the updated F1LCDx assay using Twist Fast Hyb performs per product requirements.

10 Clinical Validation Studies

10.1 Clinical Bridging Study: Detection of ALK Rearrangements to Determine Eligibility for Treatment with Alectinib

The clinical validity of using FoundationOne Liquid CDx as a companion diagnostic to identify patients with non- small cell lung cancer (NSCLC) harboring *ALK* rearrangements for treatment with alectinib was assessed through a clinical bridging study using screening (i.e., pre-alectinib treatment) plasma samples from Cohort A of the Blood First Assay Screening Trial (BFAST, BO29554).

The BFAST trial is a Phase II/III multicenter study, in which Cohort A evaluated the safety and efficacy of alectinib as a treatment for patients with advanced or metastatic NSCLC who tested positive for an *ALK* rearrangement as determined by a blood-based NGS clinical trial assay (CTA).

The concordance between FoundationOne Liquid CDx and the CTA was evaluated as summarized in **Table 43**.

Table 43. Concordance between FoundationOne Liquid CDx and the CTA for the detection of ALK rearrangements

	CTA Pos	CTA Neg	Total
FoundationOne Liquid CDx Positive ¹	63	0	63
FoundationOne Liquid CDx Negative	12	174	186
Missing	4	9	13
Total	79	183	262

¹ VAF values down to 0.06%VAF were observed for *ALK* rearrangements.

The PPA and NPA between FoundationOne Liquid CDx and the CTA using the CTA as the reference for the primary analysis set and the corresponding 95% confidence intervals were:

- PPA [95% CI]: 84.0% [73.7%, 91.4%]
- NPA [95% CI]: 100% [97.9%, 100.0%]

After adjusting for a 5% prevalence of *ALK* rearrangements in the intended use population, the PPV and NPV calculated using the CTA as the reference and the corresponding 95% confidence intervals were:

- PPV [95% CI]: 100.0% [94.3%, 200.0%]
- NPV [95% CI]: 93.5% [89.0%, 96.6%]

The estimated Overall Response Rate (ORR) and the corresponding 95% confidence intervals was 88.9% [78.4%, 95.4%] for the FoundationOne Liquid CDx *ALK*-positive population which is comparable with the observed ORR and the corresponding 95% confidence intervals of 87.4% [78.5%, 93.5%] for the CTA *ALK*- positive population (BFAST Cohort A).

A sensitivity analysis was performed to estimate the clinical efficacy of treating patients with alectinib when considering missing FoundationOne Liquid CDx results. The estimated ORR and the corresponding 95% confidence intervals were 90.4% [90.1%, 90.6%] for the patient population that are both CTA *ALK*+ and FoundationOne Liquid CDx *ALK*+, demonstrating the robustness of the clinical efficacy analysis to missing FoundationOne Liquid CDx results.

10.2 FoundationOne Liquid CDx Concordance Study for EGFR exon 19 deletion and EGFR exon 21 L858R Alteration

Clinical validity of FoundationOne Liquid CDx assay was established as a companion diagnostic to identify patients with advanced NSCLC who may be eligible for treatment with TARCEVA® (erlotinib), IRESSA® (gefitinib), or TAGRISSO® (osimertinib). Two hundred and eighty retrospective samples from NSCLC patients were included in this study, which were tested for *EGFR* exon 19 deletion and exon 21 L858R alterations (*EGFR* alterations) by the FoundationOne Liquid CDx assay and the previously approved **cobas®** *EGFR* Mutation Test v2 (Roche Molecular Systems, referred to as cobas assay). Both *EGFR* alteration-positive and *EGFR* alteration-negative samples (based on CTA results) were selected from the screen failed population of an unrelated clinical trial in NSCLC. To avoid selection bias, the samples were selected starting with a specific testing date until the predefined number of 150 *EGFR* alteration-positive and 100 *EGFR* alteration-negative samples were fulfilled. Samples were tested across two replicates by the cobas assay (denoted as CCD1 and CCD2) and one replicate by FoundationOne Liquid CDx. The tested samples, from NSCLC patients, were compared against the intended use (IU) population with respect to gender to ensure the screening population is representative of the IU population. The variant calls were evaluated based on the agreement between both the FoundationOne Liquid CDx and the cobas assay results and between the two cobas assay replicates. For any samples in which there was insufficient plasma to process both CCD1 and CCD2, processing was not performed. In total there were 177 samples with complete test results available for analysis. The agreement analysis results between FoundationOne Liquid CDx and the cobas assay for the detection of *EGFR* exon 19 deletions and L858R alterations are presented in **Table 44**.

Table 44. Agreement analysis results for EGFR exon 19 deletion and L858R separately.

Exon 19 deletion	PPAC1F	95.5%	NPAC1F	95.6%
	PPAC1C2	97.7%	NPAC1C2	98.9%
	PPAC2F	95.5%	NPAC2F	96.0%
	PPAC2C1	96.2%	NPAC2C1	99.4%
L858R	PPAC1F	100.0%	NPAC1F	95.6%
	PPAC1C2	92.9%	NPAC1C2	98.9%
	PPAC2F	100.0%	NPAC2F	94.7%
	PPAC2C1	96.0%	NPAC2C1	98.0%

The concordance of *EGFR* mutations as detected by FoundationOne Liquid CDx and the cobas assay were assessed and the data are summarized in **Table 45**.

Table 45. Concordance among CCD1, CCD2 and FoundationOne Liquid CDx results with eligible samples (n=177)

	CCD1+			CCD1-		
	CCD2+	CCD2-	Total	CCD2+	CCD2-	Total
FoundationOne Liquid CDx+	80	4	84	1	3	4
FoundationOne Liquid CDx-	2	0	2	0	87	87
Total	82	4	86	1	90	91

The agreement analysis results between FoundationOne Liquid CDx and the cobas assay are presented in **Table 46**.

Table 46. Agreement analysis results

	PPA	NPA
CCD2 CCD1 ¹	95.3%	98.9%
CCD1 CCD2 ²	96.1%	98.7%
FoundationOne Liquid CDx CCD1*	97.7%	95.6%
FoundationOne Liquid CDx CCD2**	97.7%	95.4%

¹CCD1: the 1st replicate of cobas assay as the reference

²CCD2: the 2nd replicate of cobas assay as the reference

The estimates of ζ PPA1, ζ PPA2, ζ NPA1 and ζ NPA2 and the corresponding one-sided 95% upper bounds confidence limit computed using the bootstrap method are presented in **Table 47**.

Table 47. Point estimate and one-Sided 95% upper confidence limit of ζ PPA1, ζ NPA1, ζ PPA2, and ζ NPA

	Point Estimate	Mean one-sided 95% upper confidence limit
ζ PPA1	-2.3%	2.3%
ζ NPA1	3.3%	6.6%
ζ PPA2	-1.6%	4.7%
ζ NPA2	3.3%	6.6%

Based on these results, FoundationOne Liquid CDx has been demonstrated to be non-inferior to the cobas assay for the detection of *EGFR* exon 19 deletions and *EGFR* exon 21 L858R mutations. This study establishes the clinical validity of the FoundationOne Liquid CDx assay for identifying patients eligible for treatment with erlotinib, gefitinib, and osimertinib.

10.3 Clinical Bridging Study: Detection of BRCA1/BRCA2/ATM Alterations to Determine Eligibility for Treatment with olaparib

The clinical validity of using FoundationOne Liquid CDx as a companion diagnostic to identify patients with metastatic castrate-resistant prostate cancer (mCRPC) harboring *BRCA1*, *BRCA2* or *ATM* alterations for treatment with olaparib was assessed through a clinical bridging study using screening (i.e., pre-olaparib treatment) plasma samples from Cohort A of the PROfound trial.

The PROfound trial is a Phase III, open label, randomized study to assess the efficacy and safety of olaparib (Lynparza™) versus enzalutamide or abiraterone acetate in men with metastatic castration-resistant prostate cancer who have failed prior treatment with a new hormonal agent and have homologous recombination repair gene mutations. Only Cohort A patients with either *BRCA1*, *BRCA2* or *ATM* mutations were tested with the FoundationOne Liquid CDx assay.

In total, 4,425 patients were screened and 387 (9.6%) were randomized into the PROfound study by the CTA. Of these 387 patients, 245 patients were randomized in cohort A. In cohort A, 181 out of the 245 randomized patients both consented to the use of their sample for ctDNA CDx development and had a plasma sample available for testing. In total, 181/245 (73.9%) of the Cohort A patients were tested using the FoundationOne Liquid CDx assay. Of these, 139 (76.8%) Cohort A patients had a successful FoundationOne Liquid CDx test result and 42 Cohort A patients had a failed FoundationOne Liquid CDx test result. This represents 56.7% (139/245) of total Cohort A patients with a FoundationOne Liquid CDx result. In addition, 250 non-HRRm patient samples were randomly selected for ctDNA testing from the screen-failed population to determine the NPA/NPV of the FoundationOne Liquid CDx assay. A total of 194/250 (77.6%) screen failed non-HRRm patients were successfully tested using the

FoundationOne Liquid CDx assay.

Of the 139 successfully tested Cohort A patients, 111 patients were reported as *BRCA1/BRCA2/ATM* mutation positive and 28 randomized patients were reported as biomarker negative by FoundationOne Liquid CDx.

Therefore, the FoundationOne Liquid CDx ctDNA biomarker positive subgroup comprises 111 patients with *BRCA1*, *BRCA2*, and/or *ATM* mutations.

Table 48. Sample accountability for olaparib clinical bridging study

Description	Number of patients
Patients randomized into PROfound	387
Patients with qualifying <i>BRCA1</i> , <i>BRCA2</i> , or <i>ATM</i> alterations (Cohort A)	245
Cohort A patients with samples tested by FoundationOne Liquid CDx	181
FoundationOne Liquid CDx results available	139
Cohort A patients, biomarker positive by FoundationOne Liquid CDx	111

Table 49 shows the agreement analysis between CLIA CTA (tissue test) and the FoundationOne Liquid CDx results for PROfound patients, including Invalid and Not Tested results.

Table 49. Summary of agreement analyses for FoundationOne Liquid CDx compared against CTA tissue test

		CTA Results (n=495)	
		Biomarker positive	Biomarker negative
FoundationOne Liquid CDx assay	Biomarker positive ¹	111	16
	Biomarker ² negative	28	178
	Biomarker ³ Invalid	42	56
	Not Tested	64	0
Agreement analyses (only Valid results included)	PPA (95% CI ³)	79.9 (72.2, 86.2) [111/139]	
	NPA (95% CI ³)	91.8 (87.0, 95.2) [178/194]	
	OPA (95% CI ³)	86.8 (82.7, 90.2) [289/333]	
	PPV (95% CI ³)	66.6 (56.0, 77.2)	
	NPV (95% CI ³)	95.7 (94.3, 97.1)	

¹ VAF values down to 0.11% VAF were observed for short variants and 0.25% VAF for rearrangements in *BRCA1*, *BRCA2*, or *ATM*.

² Biomarker refers to patients with eligible *BRCA/ATM* mutations

³ Confidence intervals calculated using Clopper-Pearson method

The PPA and NPA between FoundationOne Liquid CDx and the CTA using the CTA as the reference for the primary analysis set and the corresponding 95% confidence intervals were:

- PPA [95% CI]: 79.9% [72.2%, 86.2%]
- NPA [95% CI]: 91.8% [87.0%, 95.2%]

After adjusting for a 17.1% prevalence of *BRCA1/2* and *ATM* alterations in the intended use population, the PPV and NPV calculated using the CTA as the reference and the corresponding 95% confidence intervals were:

- PPV [95% CI]: 66.6% [56.0%, 77.2%]
- NPV [95% CI]: 95.7% [94.3%, 97.1%]

The estimated radiological progression-free survival (rPFS) hazard ratio (HR) and the corresponding 95% confidence intervals were 0.331 [0.21, 0.53] for the FoundationOne Liquid CDx biomarker positive population, which were comparable with the observed rPFS HR and the corresponding 95% confidence intervals of 0.34 [0.25, 0.47] for the CTA biomarker positive population (PROfound Cohort A).

Sensitivity analysis to evaluate the robustness of the clinical efficacy estimate against the unknown FoundationOne Liquid CDx results was performed using the multiple imputation method in All Patients. After imputing the missing FoundationOne Liquid CDx results, the median rPFS HR and corresponding [95% CI] across the imputed datasets was 0.44 [0.32, 0.59], demonstrating robustness of the analysis to missing FoundationOne Liquid CDx results.

10.4 Clinical Bridging Study: Detection of BRCA1 and BRCA2 Alterations to Determine Eligibility of mCRPC Patients for Treatment with rucaparib

The clinical performance of FoundationOne Liquid CDx as a companion diagnostic to identify patients with metastatic castration-resistant prostate cancer (mCRPC) harboring breast cancer gene 1 or 2 (*BRCA1* or *BRCA2*) alterations for treatment with rucaparib was demonstrated using pre-rucaparib treatment blood samples from clinical trial NCT0952534 (TRITON2). The clinical data supporting the use of rucaparib in the proposed indication was submitted as New Drug Application (NDA) 209115/S-004.

A bridging study was conducted to evaluate: 1) the concordance between *BRCA1* and *BRCA2* alteration status by the CTA and FoundationOne Liquid CDx, and 2) the clinical efficacy of rucaparib treatment in patients that would be eligible for therapy based on *BRCA1* and *BRCA2* alteration status as determined by FoundationOne Liquid CDx. A total of 209 patients (All Patients) from TRITON2 were included in NDA 209115/S-004. Genomic status was determined using the FoundationOne LDT (F1 LDT), the FoundationOne Liquid LDT, or a local test, as summarized in **Figure 1**.

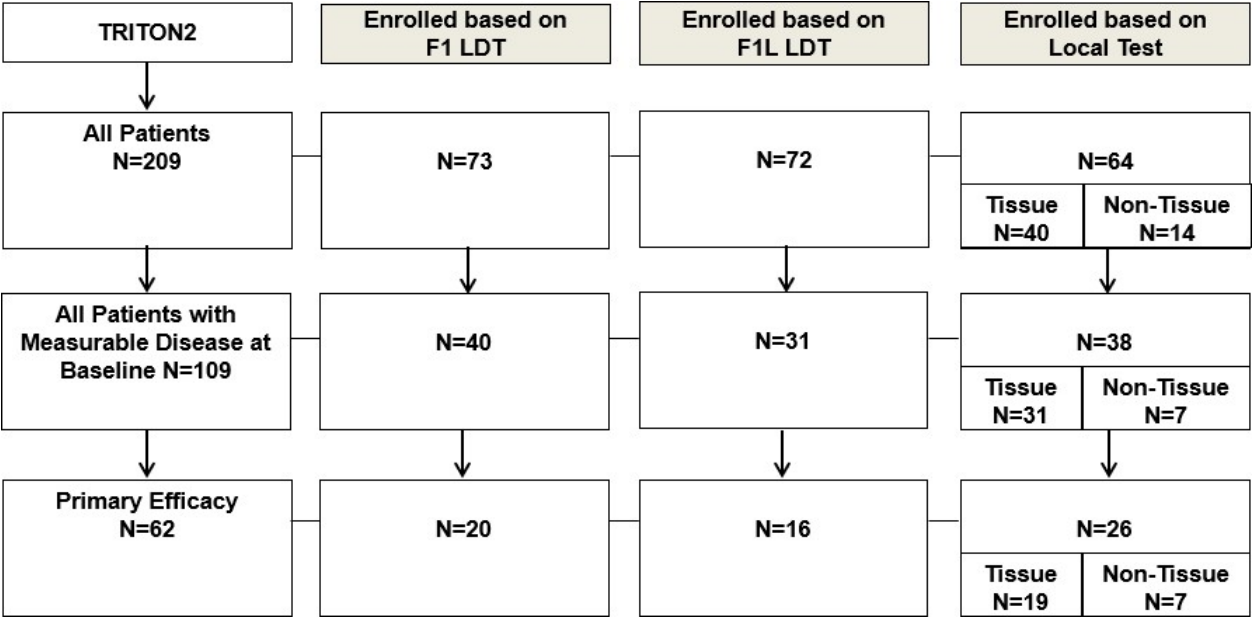


Figure 1: TRITON2 Patient Enrollment

Pre-rucaparib treatment plasma samples were available for 92% (192/209) of the patients. FoundationOne Liquid CDx data were available for 93% (178/192) of the patients with samples tested; inadequate input material resulted in FoundationOne Liquid CDx test data being unavailable for 14

patients. In total, FoundationOne Liquid CDx data were available for 85% (178/209) of All Patients.

Of the 62 patients in the Primary Efficacy Population (those patients with measurable visceral and/or nodal disease at baseline), FoundationOne Liquid CDx test data were obtained for 84% (52/62) and used for concordance and efficacy analyses. The sample accountability for this clinical bridging study is summarized in **Table 50**.

Table 50. Sample accountability for rucaparib prostate clinical bridging study

Description	Number
All Patients in TRITON2	209
Total samples available for retesting by FoundationOne Liquid CDx	192
Patients with evaluable FoundationOne Liquid CDx data and cfDNA input $\geq$ 30ng (All Patients)	161
Patients with evaluable FoundationOne Liquid CDx test results and cfDNA input $\geq$ 20ng (All Patients)	178
Primary efficacy population in TRITON2	62
Patients with evaluable FoundationOne Liquid CDx test results and cfDNA input $\geq$ 30ng (Primary Efficacy Population)	48
Patients with evaluable FoundationOne Liquid CDx test results and cfDNA input $\geq$ 20ng (Primary Efficacy Population)	52

Concordance between FoundationOne Liquid CDx and the CTAs

The concordance of *BRCA* status between FoundationOne Liquid CDx and CTA test results were evaluated in all patients as summarized in **Table 51** and **Table 52**.

Table 51. Concordance between FoundationOne Liquid CDx BRCA Status and the CTA BRCA Status in All Patients with FoundationOne Liquid CDx cfDNA input $\geq$ 30ng

All Patients		CTA		
		BRCA Positive	BRCA Negative	Total
FoundationOne Liquid CDx	BRCA Positive ¹	75	1	76
	BRCA Negative	16	69	85
	BRCA Unknown	2	1	3
	Total	93	71	164

¹ VAF values down to 0.15%VAF were observed for short variants and 0.85%VAF for rearrangements in *BRCA1* or *BRCA2*.

The PPA, NPA between FoundationOne Liquid CDx and the CTA, based on a cfDNA input $\geq$ 30ng, were determined using the CTA as the reference for all patients.

- PPA (95% CI): 82.4% (73.0%, 89.6%)
- NPA (95% CI): 98.6% (92.3%, 100.0%)

Table 52. Concordance between FoundationOne Liquid CDx BRCA Status and the CTA BRCA Status in All Patients with FoundationOne Liquid CDx cfDNA input $\geq$ 20ng

All Patients		CTA		
		BRCA Positive	BRCA Negative	Total
FoundationOne Liquid CDx	BRCA Positive ¹	82	1	83
	BRCA Negative	18	77	95
	BRCA Unknown	3	2	5
	Total	103	80	183

¹ VAF values down to 0.15%VAF were observed for short variants and 0.85%VAF for rearrangements in *BRCA1* or *BRCA2*.

The PPA, NPA between FoundationOne Liquid CDx and the CTA, based on a cfDNA input ≥ 20 ng, were determined using the CTA as the reference for all patients.

- PPA (95% CI): 82.0% (73.1%, 89.0%)
- NPA (95% CI): 98.7% (93.1%, 100%)

Efficacy Based on FoundationOne Liquid CDx Results

BRCA1 and *BRCA2* alteration status were verified retrospectively by FoundationOne Liquid CDx in 66% (41/62) of the patients in the Primary Efficacy Population. The ORR [95% CI] in the Primary Efficacy Population was 46.3% [30.7%-62.6%] in *BRCA* positive patients determined by FoundationOne Liquid CDx, which is comparable to the ORR of 43.5% [31.0%-56.7%] in patients identified by CTA (**Table 53**).

Table 53. ORR in the primary efficacy population by CTA and FoundationOne Liquid CDx test results

Primary Efficacy Population	FoundationOne Liquid CDx		CTA
	<i>BRCA</i> Positive N=38 (≥ 30 ng cfDNA input)	<i>BRCA</i> Positive N = 41 (≥ 20 ng cfDNA input)	<i>BRCA</i> Positive N = 62
Confirmed ORR (CR + PR), n (%)	18 (47.4)	19 (46.3)	27 (43.5)
95% CI(%)	31.0 – 64.2	30.7 - 62.6	31.0 – 56.7

ORR = objective response rate; CR = complete response; PR = partial response.

Sensitivity analysis to evaluate the robustness of the clinical efficacy estimate against the unknown FoundationOne Liquid CDx results was performed using the multiple imputation method and demonstrated that the drug efficacy in the FoundationOne Liquid CDx positive population was robust to missing FoundationOne Liquid CDx results.

10.5 Clinical Bridging Study: Detection of *PIK3CA* Alterations to Determine Eligibility for Treatment with alpelisib

Clinical validity of using FoundationOne Liquid CDx to identify breast cancer patients harboring *PIK3CA* alterations eligible for treatment with alpelisib was assessed through retrospective testing of plasma samples collected prior to study treatment from advanced or metastatic breast cancer patients enrolled in clinical trial CBYL719C2301 (SOLAR-1). A total of 395 patients were enrolled based on CTA1 results and 177 patients were enrolled based on CTA2 results. All 395 patients enrolled based on CTA1 results were retrospectively tested by CTA2. This clinical bridging study was performed based on CTA2 results.

Samples with ≥ 30 ng from 375 patients were tested by FoundationOne Liquid CDx. Excluding those with invalid results for either CTA2 or CDx (4 and 12, respectively), the primary efficacy analyses were conducted using data from the 359 subjects who were CTA2-evaluable and CDx-evaluable **Table 54**.

Table 54. Concordance between FoundationOne Liquid CDx and CTA2

CDx	CTA2			Total
	Positive	Negative	Invalid	
Positive	165	0	1	166
Negative	65	129	3	197
Invalid	7	5	0	12
Total	237	134	4	375

¹ VAF values down to 0.14% VAF were observed for short variants in *PIK3CA*. Samples not tested are excluded from the analysis. Samples tested with cfDNA input <30 ng are excluded from the analysis.

The point estimates of PPA and NPA between FoundationOne Liquid CDx and the CTA2 assay and the corresponding 95% confidence intervals were:

- PPA [95% CI]: 71.7% [65.4%, 77.5%]
- NPA [95% CI]: 100% [97.2%, 100%]

The primary efficacy analysis in the *PIK3CA* alteration positive population identified by FoundationOne Liquid CDx was based on PFS by local investigator assessment per Response Evaluation Criteria in Solid Tumors (RECIST) 1.1 criteria. Clinical efficacy of alpelisib in combination with fulvestrant for the FoundationOne Liquid CDx-positive population with cfDNA input ≥ 30 ng (N=165) was demonstrated with an estimated 54% risk reduction in disease progression or death in the alpelisib plus fulvestrant arm compared to the placebo plus fulvestrant arm (HR = 0.46, 95% CI: 0.30, 0.70).

As summarized in **Table 55**, the PFS hazard ratio for the 165 tissue CTA2-positive, FoundationOne Liquid CDx- positive patients was 0.46 (95% CI: 0.30, 0.70). Median PFS was 11.0 months for the alpelisib plus fulvestrant arm versus 3.6 months for the placebo plus fulvestrant arm.

Table 55. Progression-free survival in the CTA2-positive, FoundationOne Liquid CDx-positive patients (primary analysis set)

Progression free survival (months)	Alpelisib 300mg qd + Fulvestrant N=84	Placebo qd + Fulvestrant N=81	HR (95% CI) Alpelisib 300mg qd + Fulv /Placebo qd + Fulv ¹
No of events (%)	54 (64.3)	67 (82.7)	0.46 (0.30, 0.70)
PD (%)	52 (61.9)	61 (75.3)	
Death (%)	2 (2.4)	6 (7.4)	
No of censored (%)	30 (35.7)	14 (17.3)	
Median (95% CI) ²	11.0 (7.3, 15.9)	3.6 (2.4, 5.8)	

¹ Hazard ratio (HR) estimated using Cox regression model stratified by the two stratification factors: presence of lung and/or liver metastases, previous treatment with any CDK4/6 inhibitor, and adjusted for clinically relevant covariates, as well as the imbalanced covariates.

² The 95% CI calculated from PROC LIFETEST output using the method of Brookmeyer and Crowley (1982). CDx results from samples tested with cfDNA input <30 ng are treated as missing.

PD = progressive disease

Sensitivity analysis to evaluate the robustness of the clinical efficacy estimate against the missing FoundationOne Liquid CDx results was performed using the multivariate imputation by chained equations (MICE) method. After imputing the missing FoundationOne Liquid CDx results, the hazard ratio was estimated to be 0.63 (95% CI: 0.45, 0.87), demonstrating robustness of the clinical efficacy analysis to missing FoundationOne Liquid CDx results.

10.6 Clinical Bridging Study: Detection of MET single nucleotide variants (SNVs) and indels that lead to MET exon 14 skipping to Determine Eligibility for Treatment with capmatinib

The clinical performance of FoundationOne Liquid CDx for detecting SNVs and indels that lead to *MET* exon 14 skipping in NSCLC patients who may benefit from treatment with capmatinib (**Table 1**) was established with clinical data generated from a clinical bridging study using samples from patients enrolled in the GEOMETRY mono-1 study. The study demonstrates concordance between the enrollment assay, i.e., CTA, and the FoundationOne Liquid CDx assay and establish the effectiveness of the FoundationOne Liquid CDx assay.

GEOMETRY mono-1 was a prospectively designed, multi-center, open-label, single arm Phase II study of oral cMET inhibitor, TABRECTA (capmatinib), in adult patients with *EGFR* wild-type (wt), and anaplastic lymphoma kinase (ALK) negative advanced NSCLC. Patients were enrolled into multiple

cohorts of the study, but the bridging study was focused on the fully-enrolled *MET* exon 14 skipping positive Cohorts 4 and 5b. Cohort 4 only enrolled pretreated (second and third line) patients with *MET* exon 14 skipping, and Cohort 5b only enrolled treatment-naïve patients with *MET* exon 14 skipping. Patients were screened for enrollment into Cohorts 4 and 5b for *MET* exon 14 skipping status using a *MET* exon 14 skipping reverse-transcriptase PCR (RT-PCR) CTA that was detected *MET* exon 14 skipping in a patient's tissue. Plasma samples were collected and stored prior to study treatment for retrospective testing. Patients enrolled in Cohorts 4 and 5b received 400mg of capmatinib orally twice daily in tablet form. Efficacy was evaluated every six weeks from the first day of treatment until RECIST 1.1 disease progression.

A clinical bridging study was conducted to evaluate: 1) the concordance between *MET* single nucleotide variants (SNVs) and indels that lead to *MET* exon 14 skipping status by the CTA and FoundationOne Liquid CDx, and 2) the clinical efficacy of capmatinib treatment in patients that would be eligible for therapy based on *MET* biomarker positive status as determined by FoundationOne Liquid CDx.

The primary endpoint of GEOMETRY mono-1 was the ORR by Blinded Independent Review Committee (BIRC) assessment by cohort to determine whether treatment with capmatinib is effective. Duration of response (DOR) as assessed by BIRC was the key secondary endpoint.

The primary concordance analysis of the status of *MET* SNVs and indels that led to *MET* exon 14 skipping between FoundationOne Liquid CDx and the tissue CTA test results were evaluated in both analysis sets that met ≥ 30 ng cfDNA input and ≥ 20 ng cfDNA input. The analysis on the ≥ 30 ng cfDNA input population evaluated 150 patients (78 *MET* exon 14 skipping positive patients, and 72 *MET* exon 14 skipping negative patients), excluding invalid CDx results. The analysis on the ≥ 20 ng cfDNA input population evaluated 171 patients (83 *MET* exon 14 skipping positive patients, and 88 *MET* exon 14 skipping negative patients), excluding invalid CDx results.

Agreement (PPA, NPA and OPA) for combined Cohort 4 and 5b by ≥ 30 ng cfDNA input and ≥ 20 ng cfDNA input CDx are shown in **Table 56** and **Table 57**, below. For the 150 patients meeting the ≥ 30 ng cfDNA input, the PPA, NPA and OPA and respective confidence intervals were determined to be 70.5% (59.1%, 80.3%), 100% (95.0%, 100%) and 84.7% (77.9%, 90.0%). For the 171 patients meeting the ≥ 20 ng cfDNA input, the PPA, NPA and OPA and respective confidence intervals were determined to be 68.7% (57.6%, 78.4%), 100% (95.9, 100%) and 84.8% (78.5%, 89.8%).

Table 56. Agreement between CDx and CTA based on CTA results in combined cohorts by cfDNA input ≥ 30 ng

Cohort 4 and Cohort 5b (CDx sample requirement: cfDNA input ≥ 30 ng)	Measure of agreement	Percent agreement % (n/N)	95% CI (1)
	PPA ¹	70.5 (55/ 78)	(59.1, 80.3)
	NPA	100 (72/ 72)	(95.0, 100)
	OPA	84.7 (127/150)	(77.9, 90.0)

¹ VAF values down to 0.16%VAF were observed for *MET* short variants.

N: The total number of patients. It is the denominator for percentage (%) calculation n: Number of patients with agreement between CTA and CDx

(1) The 95% CI calculated using Clopper-Pearson method

Table 57. Agreement between CDx and CTA based on CTA results in combined cohorts by cfDNA input ≥ 20 ng

Cohort 4 and Cohort 5b (CDx sample requirement: cfDNA input ≥ 20 ng)	Measure of agreement	Percent agreement % (n/N)	95% CI (1)
	PPA ¹	68.7 (57/ 83)	(57.6, 78.4)

	NPA	100 (88/ 88)	(95.9, 100)
	OPA	84.8 (145/171)	(78.5, 89.8)

¹ VAF values down to 0.16%VAF were observed for *MET* short variants.

N: The total number of patients. It is the denominator for percentage (%) calculation n: Number of patients with agreement between CTA and CDx

(1) The 95% CI calculated using Clopper-Pearson method

Based on the PPA of 70.5% (59.1%, 80.3%) between FoundationOne Liquid CDx and the tissue CTA, reflex testing using tissue specimens to an FDA approved tissue test is recommended, if feasible, if the plasma test is negative.

Clinical effectiveness of FoundationOne Liquid CDx was evaluated by estimation of clinical efficacy in the CTA-enrolled *MET* exon 14 deletion positive patient population, as assessed by the primary objective of ORR by BIRC. The GEOMETRY mono-1 clinical trial met its primary objective demonstrating a statistically significant improvement in ORR by BIRC assessments in patients with *MET* exon 14 deletion positive tumors in each cohort.

Table 58 and **Table 59** present the clinical efficacy of TABRECTA analyzed in CTA-positive patients who were tested as CDx positive (“double positive” patients) in each cohort that met the ≥ 30 ng cfDNA input and ≥ 20 ng cfDNA input CDx sample requirements, respectively. In Cohort 4 there were 39 patients with ≥ 30 ng cfDNA input and 41 with ≥ 20 ng cfDNA input with valid results for analysis of ORR. In Cohort 5b there were 16 patients, all of whom met the ≥ 30 ng cfDNA input.

Patients in Cohort 4 that met the ≥ 30 ng cfDNA input demonstrated an ORR of 51.3% (34.8%, 67.6%). Patients from Cohort 4 that met the ≥ 20 ng cfDNA input requirements demonstrated an ORR of 48.8% (32.9%, 64.9%). For patients in Cohort 5b, all patients met the ≥ 30 ng cfDNA input and demonstrated an ORR of 81.3% (54.4%, 96.0%).

Table 58. Overall response per BIRC assessment in (CTA-positive, CDx-positive) and CTA- positive patients by cohort and CDx sample requirements (Cohort 4)

(CTA+, CDx+) CDx sample requirements						
	cfDNA input ≥ 30 ng N=39		cfDNA input ≥ 20 ng N=41		CTA+ N=69	
	n (%)	95% CI (1)	n (%)	95% CI (1)	n (%)	95% CI (1)
Overall Response Rate (ORR: CR + PR)	20 (51.3)	(34.8, 67.6)	20 (48.8)	(32.9, 64.9)	28 (40.6)	(28.9, 53.1)

(1) The 95% CI calculated with the Clopper-Pearson Exact method.

Table 59. Overall response per BIRC assessment in (CTA-positive, CDx-positive) and CTA- positive patients by cohort and CDx sample requirements (Cohort 5b).

(CTA+, CDx+) CDx sample requirements						
	cfDNA input ≥ 30 ng N=16		cfDNA input ≥ 20 ng N=16		CTA+ N=28	
	n (%)	95% CI (1)	n (%)	95% CI (1)	n (%)	95% CI (1)
Overall Response Rate (ORR: CR + PR)	13 (81.3)	(54.4, 96.0)	13 (81.3)	(54.4, 96.0)	19 (67.9)	(47.6, 84.1)

(1) The 95% CI calculated with the Clopper-Pearson Exact method.

Estimated drug efficacy in FoundationOne Liquid CDx Positive (F1LCDx(+)) patients

The ORR by BIRC assessment in F1LCDx(+) patients was calculated for Cohort 4 and Cohort 5b, separately. Because all CTA(-) patients are tested as negative by CDx (i.e. NPA=100%) and thus PPV is estimated as 100%, the results do not vary with Pr(CTA+) values and the ORR in F1LCDx(+)

population is estimated as the same as the ORR in the FoundationOne Liquid CDx [CTA(+)/CDx(+)] population. For F1LCDx(+) patients meeting “Recommended” CDx sample requirement (cfDNA input ≥ 30 ng), the ORR (95% CI) is 51.3% (34.8%, 67.6%) in Cohort 4 and 81.3% (54.4%, 96.0%) in Cohort 5b, respectively. For CDx(+) patients meeting “Minimum” CDx sample requirement (cfDNA input ≥ 20 ng), the ORR (95% CI) is 48.8% (32.9%, 64.9%) in Cohort 4 and 81.3% (54.4%, 96.0%) in Cohort 5b, respectively.

Sensitivity analysis on missing FoundationOne Liquid CDx results

The impact of missing FoundationOne Liquid CDx results on the concordance between CTA and FoundationOne Liquid CDx and final drug efficacy in F1LCDx(+) patients was evaluated by imputing the missing FoundationOne Liquid CDx results using multiple imputation method. For Cohort 4, the imputed ORR (95% CI) by BIRC were estimated to be 46.5% (32.6%, 60.9%) given “Recommended” sample requirement and 47.2% (33.3%, 61.5%) given “Minimum” sample requirement. For Cohort 5b, the imputed ORRs and two-sided 95% CIs by BIRC were estimated to be 75.3% (53.3%, 94.4%) given “Recommended” sample requirement and 78.1% (55.6%, 95.5%) given “Minimum” sample requirement. The sensitivity analysis results demonstrated that the concordance between CTA and FoundationOne Liquid CDx and final drug efficacy in F1LCDx(+) population are robust to missing FoundationOne Liquid CDx results.

10.7 Clinical Bridging Study: Detection of ROS1 Fusions to Determine Eligibility for Treatment with entrectinib

The clinical performance of using FoundationOne Liquid CDx as a companion diagnostic to identify NSCLC patients harboring *ROS1* fusions eligible for treatment with entrectinib (**Table 1**) was assessed in this clinical bridging study. All available pre-entrectinib treatment plasma samples from patients enrolled in ALKA, STARTRK-1, and STARTRK-2 clinical trials were tested by FoundationOne Liquid CDx as part of this clinical bridging study. Only samples from STARTRK-2 were available for testing by FoundationOne Liquid CDx.

A clinical bridging study was conducted to evaluate the 1) the concordance between the FoundationOne Liquid CDx assay and the CTAs used for clinical trial enrollment for the detection of *ROS1* fusions and 2) the clinical efficacy of entrectinib treatment in patients who would be eligible for therapy based on *ROS1* fusions positive as determined by FoundationOne Liquid CDx.

A total of 255 patients were included in the clinical bridging study. Of these 255 patients, 161 were determined as *ROS1* fusion positive based on testing by the CTAs. Initially, the clinical bridging study included 51 *ROS1* fusion positive NSCLC patients from the new drug application (NDA) efficacy population, 41 additional *ROS1* fusion positive, *ROS1* inhibitor-naïve patients with NSCLC with measurable disease who had insufficient follow-up (<12 months) at the time of the NDA submission, 67 *ROS1* fusion positive patients with NSCLC who were enrolled prior to October 31, 2018, and two patients with prior *ROS1* inhibitor treatment and used only for the concordance evaluation. In total, clinical outcome data from 161 *ROS1* fusion positive patients (as determined by the CTAs) enrolled before October 31, 2018 (based on the May 1, 2019 clinical data cutoff date) were planned for use in the bridging analysis. Of the 94 *ROS1* fusion negative samples (as determined by the CTAs), 73 were patients enrolled in the clinical trial by the CTAs as *NTRK1/2/3* fusion positive. The remaining 21 *ROS1* fusion negative samples were FFPE tissue-matched plasma samples procured from a commercial source, with tissue testing by one of the CTAs used for clinical trial enrollment. Only samples from STARTRK-2 were available for testing by FoundationOne Liquid CDx and, thus, 218 of the 255 samples were evaluated by retrospective FoundationOne Liquid CDx testing. Among them, 203 samples met the FoundationOne Liquid CDx quality control metrics, and 175 samples met the recommended sample input of cfDNA ≥ 30 ng. An additional 28 samples met the minimum FoundationOne Liquid CDx sample input criteria of cfDNA ≥ 20 ng. Sample accountability for this clinical bridging study is summarized in

Table 60.

Table 60. Sample Accountability for the ROS1 Clinical Bridging Study

Source of samples	Total # of samples (n=255)	Sample fail/unavailable (n=52)	F1LCDx evaluable (n=203)	DNA ≥ 30 ng (n=175)	DNA ≥ 20 ng and < 30 ng (n=28)
Procured <i>ROS1</i> Negative samples	21	2	19	17	2
<i>ROS1</i> Negative by CTA test*	73	14	59	51	8
<i>ROS1</i> Positive by CTA test	161	36	125	107	18
Total	255	52 (20.4%)	203 (79.6%)	175 (68.6%)	28 (11.0%)

*The CTA *ROS1*-fusion negative samples were enrolled in the clinical trials as CTA *NTRK*-fusion positive

The primary analyses were conducted for the 175 patients with evaluable FoundationOne Liquid CDx results that also had a DNA input of ≥ 30 ng. The concordance between FoundationOne Liquid CDx and the CTAs is summarized in **Table 61**. Over 20 different types of CTAs with a mix of technologies (RT-PCR, FISH, NGS) and analytes (RNA and DNA) were used to enroll the patients in the clinical trials.

Table 61. Concordance result between FoundationOne Liquid CDx and CTA for the detection of *ROS1*-fusions for samples with DNA content ≥30 ng (n=175).

		CTAs		
		Detected	Not Detected	Total
F1LCDx	Detected	55	0	55
	Not Detected	52	68	120
	Unevaluable	54	26	80
	Total	161	94	255
Agreement Statistics Excluding CDx-Unevaluable Results		PPA 51.4% (55/107) 95% CI*: (42.05%, 60.66%)	NPA 100% (68/68) 95% CI*: (94.65%, 100%)	
Percent Unevaluable		33.5% (54/161) 95% CI*: (26.7%, 41.1%)	27.7% (26/94) 95% CI*: (19.6%, 37.4%)	

*Calculated with Wilson two-sided 95% CI

The following concordance statistics were calculated for this sample set using the CTA as the reference:

- PPA [95% CI]: 51.4% [42.05%, 60.66%]
- NPA [95% CI]: 100.0% [94.65%, 100%]

After adjusting for a 1% prevalence of *ROS1* rearrangements in the intended use population PPV and NPV were calculated using the CTA as the reference:

- PPV [95% CI]: 100% [93.47%, 100%]
- NPV [95% CI]: 99.51% [99.41%, 99.61%]

The discordances between the CTAs and FoundationOne Liquid CDx among *ROS1* fusion positive patients was evaluated by stratifying the PPA into 2 subgroups, DNA-based NGS CTAs and RNA-based NGS CTAs. The PPA between FoundationOne Liquid CDx and DNA-based NGS CTAs was 55.6% (10/18) with 95% two-sided CI (33.7%, 75.4%). The PPA between FoundationOne Liquid CDx and RNA-based NGS CTAs was 50.6% (40/79) with 95% two-sided CI (39.8%, 61.4%). Of the 52 CTA positive patients who were FoundationOne Liquid CDx negative, 92.3% (48/52) did not have detectable tumor fraction as determined by FoundationOne Liquid CDx, suggesting that the ctDNA content in these

samples was low.

The clinical efficacy of entrectinib in the clinical trials was measured in ORR with either confirmed complete response (CR) or partial response (PR) based on blinded independent centralized review (BICR). Only clinical samples with clinical outcome data were used in this part of the study analysis.

The ORR in the CTA-positive population was 67.3% (107/159) with 95% two-sided CI (59.7%, 74.1%). Fifty-four patients were CTA positive and had FoundationOne Liquid CDx *ROS1* fusion-positive results. The ORR for this population was 66.7% (36/54) with 95% two-sided CI (53.4%, 77.8%). Fifty-one patients were CTA positive but had FoundationOne Liquid CDx *ROS1* negative results. The ORR for this population was 66.7% (34/51) with 95% two-sided CI (53.0%, 78.0%).

Fifty-four patients were CTA positive but were unevaluable by FoundationOne Liquid CDx. The ORR for this population was 68.5% (37/54) with 95% two-sided CI (55.3%, 79.3%) (**Table 62**).

Table 62. ORR in CTA-positive, FoundationOne Liquid CDx-positive patients

Clinical outcome	Total CTA positive population (N=159)	CTA positive and F1LCDx positive (N=54)	CTA positive and F1LCDx negative (N=51)	CTA positive and F1LCDx unevaluable (N=54)
ORR% [95% CI**]	67.3%	66.7%	66.7%	68.5%
	[59.7%, 74.1%]	[53.4%, 77.8%]	[53.0%, 78.0%]	[55.3%, 79.3%]
Complete response	14 (8.8%)	5 (9.3%)	6 (11.8%)	3 (5.6%)
Partial response	93 (58.5%)	31 (57.4%)	28 (54.9%)	34 (63.0%)
Number of responders	N=107	N=36	N=34	N=37
Duration of response				
Median [±] in months (range)	9.5 (1.8, 42.3)	6.4 (1.8, 20.5)	13.4 (1.9, 27.6)	11.1 (4.6, 42.3)
% with duration ≥9 months	61.7%	38.9%	70.6%	75.7%
% with duration ≥12 months	41.1%	19.4%	55.9%	48.6%
% with duration ≥18 months	19.6%	5.6%	26.5%	27.0%

**Two-sided 95% CI for each subgroup was based on the Wilson-score method

±Arithmetic median used (not Kaplan-Meier methods) since censoring data was not available

Sensitivity analysis to evaluate the robustness of the clinical efficacy estimate against the missing FoundationOne Liquid CDx results was performed using the multiple imputation method. Based on the 100 bootstrap samples with 50 times imputation estimated ORR of the FoundationOne Liquid CDx *ROS1*-positive population was 67.1% [50.7%, 78.9%].

There were 70 *ROS1* positive patients by the CTAs with partial or complete response to entrectinib, who also had an FoundationOne Liquid CDx result. Among them, only 51.4% (36/70) were positive by FoundationOne Liquid CDx (95% CI: 39.9, 62.8). There were 35 *ROS1*-positive patients by the CTAs who did not respond to entrectinib, who also had an FoundationOne Liquid CDx result (54-36=18 and 51-34=17). Among them, 51.4% (18/35) were positive by FoundationOne Liquid CDx (95% CI: 35.6, 67.0).

10.8 Clinical Bridging Study: Detection of NTRK 1/2/3 Fusions to Determine Eligibility for Treatment with entrectinib

The clinical performance of using FoundationOne Liquid CDx as a companion diagnostic to identify patients with solid tumors harboring *NTRK1*, *NTRK2*, or *NTRK3* fusions eligible for treatment with

entrectinib (**Table 1**) was assessed in this clinical bridging study. All patients with available plasma samples from the NDA population from ALKA, STARTRK-1, and STARTRK-2 clinical trials were tested by FoundationOne Liquid CDx as part of this clinical bridging study. Only samples from STARTRK-2 were available for testing by FoundationOne Liquid CDx.

A clinical bridging study was conducted to evaluate the 1) the concordance between the FoundationOne Liquid CDx assay and the CTAs used for clinical trial enrollment for the detection of *NTRK* fusions and 2) the clinical efficacy of entrectinib treatment in patients who would be eligible for therapy based on *NTRK* fusions positive as determined by FoundationOne Liquid CDx.

A total of 256 patients were included in the clinical bridging study. Of these 256 patients, 74 were determined as *NTRK* fusion-positive based on testing by the CTAs. Initially, the clinical bridging study included 54 *NTRK* fusion-positive patients from the NDA efficacy population, as well as 20 *NTRK* fusion-positive patients who were enrolled after the data cutoff. Of the 182 *NTRK* fusion-negative samples, 161 were patients enrolled in the clinical trial by the CTAs as *ROS1* fusion-positive. The remaining 21 *NTRK* fusion-negative samples were FFPE tissue-matched plasma samples procured from a commercial source, with tissue testing by one of the CTAs used for clinical trial enrollment. Only samples from STARTRK-2 were available for testing by FoundationOne Liquid CDx and, thus, 218 of the 256 samples were included for retrospective FoundationOne Liquid CDx testing. Among them, 203 samples met the FoundationOne Liquid CDx quality control metrics, and 175 samples met the recommended sample input of cfDNA ≥ 30 ng. An additional 28 samples met the minimum FoundationOne Liquid CDx sample input criteria of cfDNA ≥ 20 ng. Sample accountability for this clinical bridging study is summarized in **Table 63**.

Table 63. Sample Accountability for the NTRK Clinical Bridging Study

Source of samples	Total # of samples (n=256)	Sample fail/unavailable (n=53)	F1LCDx evaluable (n=203)	DNA ≥ 30 ng (n=175)	DNA ≥ 20 ng and < 30 ng (n=28)
Procured <i>NTRK</i> Negative samples	21	2	19	17	2
<i>NTRK</i> Negative by CTA test*	161	36	125	107	18
<i>NTRK</i> Positive by CTA test	74	15	59	51	8
Total	256	53 (20.7%)	203 (79.3%)	175 (68.4%)	28 (10.9%)

*The CTA *NTRK*-fusion negative samples were enrolled in the clinical trial as CTA *ROS1*-fusion positive.

The primary analyses were conducted for the 175 patients with evaluable FoundationOne Liquid CDx results that also had a DNA input of ≥ 30 ng. A comparison of the clinical outcomes and baseline characteristics demonstrated that the FoundationOne Liquid CDx-evaluable population was representative of the FoundationOne Liquid CDx-unevaluable population in this bridging study. The concordance between FoundationOne Liquid CDx and the CTAs is summarized in **Table 64**. Over 20 different types of CTAs with a mix of technologies (RT-PCR, FISH, NGS) and analytes (RNA and DNA) were used to enroll the patients in the clinical trials.

Table 64. Concordance between FoundationOne Liquid CDx and CTAs for the detection of NTRK1, NTRK2, and NTRK3 fusions

		CTAs		
		Detected	Not Detected	Total
F1LCDx	Detected	25	0	25
	Not Detected	26	124	150

	Unevaluable	23	58	81
	Total	74	182	256
Agreement Statistics Excluding CDx-Unevaluable Results		PPA: 49.0% (25/51) 95% CI*: (35.9%, 62.3%)	NPA: 100% (124/124) 95% CI*: (97.0%, 100%)	
Percent Unevaluable		31.1% (23/74) 95% CI*: (21.7%, 42.3%)	31.9% (58/182) 95% CI*: (25.5%, 39.0%)	

*Calculated with Wilson 2-sided 95% CI

The following concordance statistics were calculated for this sample set:

- PPA [95% CI]: 49.0% [35.9%, 62.3%]
- NPA [95% CI]: 100.0% [97.0%, 100%]

After adjusting for a 0.32% prevalence of *NTRK* fusions in the intended use population PPV and NPV were calculated using the CTA as the reference:

- PPV [95% CI]: 100% [86.7%, 100%]
- NPV [95% CI]: 99.8% [99.79%, 99.88%]

The discordances between the CTAs and FoundationOne Liquid CDx among *NTRK1/2/3* fusion-positive patients was evaluated by stratifying the PPA into 2 subgroups, DNA-based NGS CTAs and RNA-based NGS CTAs. The PPA between FoundationOne Liquid CDx and DNA-based NGS CTAs was 65.0% (13/20) with 95% two-sided CI (43.3%, 81.9%). The PPA between FoundationOne Liquid CDx and RNA-based NGS CTAs was 38.7% (12/31) with 95% two-sided CI (23.7%, 56.2%).

The clinical efficacy of entrectinib in the clinical trials was measured in ORR with either confirmed CR or PR based on BICR. Only clinical samples with clinical outcome data were used in this part of the study analysis.

The ORR in the CTA positive population was 63.5% (47/74) with 95% two-sided CI (52.1%, 73.6%). Twenty-five (25) patients were CTA positive and had FoundationOne Liquid CDx *NTRK* positive results. The ORR for this population was 72.0% (18/25) with 95% two-sided CI (52.4%, 85.7%). Twenty-six (26) patients were CTA positive but had FoundationOne Liquid CDx *NTRK* negative results. The ORR for this population was 57.7% (15/26) with 95% two-sided CI (38.9%, 74.5%).

23 patients were CTA positive but were FoundationOne Liquid CDx-unevaluable. The ORR for this population was 60.9% (14/23) with 95% two-sided CI (40.8%, 77.8%) (

Table 65).

Table 65. ORR in CTA-positive, FoundationOne Liquid CDx-positive patients

Clinical outcome	Total CTA positive population (N=74)	CTA positive and F1LCDx positive (N=25)	CTA positive and F1LCDx negative (N=26)	CTA positive and F1LCDx unevaluable (N=23)
ORR% [95% CI**]	63.5%	72.0%	57.7%	60.9%
	[52.1, 73.6]	[52.4, 85.7]	[38.9, 74.5]	[40.8, 77.8]
Complete response	5 (6.8%)	0 (0.0%)	1 (3.8%)	4 (17.4%)
Partial response	42 (56.8%)	18 (72.0%)	14 (53.8%)	10 (43.5%)
Number of responders	N=47	N=18	N=15	N=14
Duration of response				
Median [±] in months (range)	7.5 (1.4, 26.0)	5.9 (1.9, 16.6)	7.9 (1.4, 26.0)	8.3 (2.8, 25.9)
% with duration ≥9 months	44.7%	38.9%	46.7%	50.0%

Clinical outcome	Total CTA positive population (N=74)	CTA positive and F1LCDx positive (N=25)	CTA positive and F1LCDx negative (N=26)	CTA positive and F1LCDx unevaluable (N=23)
% with duration ≥ 12 months	29.8%	22.2%	40.0%	28.6%
% with duration ≥ 18 months	10.6%	0.0%	13.3%	21.4%

**Two-sided 95% CI for each subgroup was based on the Wilson-score method
 $\pm$ Arithmetic median used (not Kaplan-Meier methods) since censoring data was not available

Sensitivity analysis to evaluate the robustness of the clinical efficacy estimate against the missing FoundationOne Liquid CDx results was performed using the multiple imputation method. Based on the 100 bootstrap samples with 50 times imputation, the estimated ORR of the FoundationOne Liquid CDx *NTRK*-positive population was 67.5% [52.4%, 87.1%].

There were 33 *NTRK1/2/3*-positive patients by the CTAs with partial or complete response to entrectinib, who also had an FoundationOne Liquid CDx result. Among them, only 54.5% (18/33) were positive by FoundationOne Liquid CDx (95% CI: 38.0, 70.2). There were 18 CTA-positive patients who did not respond to entrectinib, who also had an FoundationOne Liquid CDx result (25-18=7 and 26-15=11). Among them, 38.9% (7/18) were positive by FoundationOne Liquid CDx (95% CI: 20.3, 61.4).

There were 25 patients positive for an *NTRK3* fusion in the entrectinib clinical studies. Among them, 68.0% (17/25) were negative for *NTRK3* fusions by FoundationOne Liquid CDx. Among the 17 patients who were negative for *NTRK3* fusions by FoundationOne Liquid CDx, 64.7% (11/17) had response to entrectinib. Furthermore, FoundationOne Liquid CDx detected one of seven different *NTRK3* fusions that were detected by the CTAs.

10.9 Clinical Bridging Study: Detection of BRAF V600E to Determine Eligibility for Treatment with encorafenib in combination with cetuximab

The clinical performance of FoundationOne Liquid CDx for the detection of *BRAF* V600E in plasma samples from patients with metastatic CRC for treatment with BRAFTOVI® (encorafenib) in combination with cetuximab was established through a clinical bridging study that assessed clinical efficacy of encorafenib and cetuximab in patients selected based on FoundationOne Liquid CDx results. Baseline plasma samples for patients enrolled in the BEACON (ARRAY-818-302) clinical trial were retrospectively tested by FoundationOne Liquid CDx in the bridging study. The study results demonstrate concordance between the CTA and the FoundationOne Liquid CDx assay, and establishes the clinical effectiveness of the FoundationOne Liquid CDx assay in identifying metastatic CRC patients with *BRAF* V600E for treatment with encorafenib in combination with cetuximab.

The BEACON trial was a randomized, open-label, multi-center, parallel group, three-arm Phase 3 study in patients with *BRAF* V600E in CRC whose disease had progressed after 1 or 2 prior regimens in the metastatic setting. The study compared the efficacy and safety of binimetinib + encorafenib + cetuximab (Triplet Arm), and encorafenib + cetuximab (Doublet Arm) to irinotecan/cetuximab or FOLFIRI/cetuximab (Control Arm).

The supplemental new drug application population included enrolled patients from the Control and Doublet arms from BEACON. The clinical trial tested the efficacy of therapy with these drugs by screening for and selecting metastatic CRC patients that harbor the *BRAF* V600E using the CTA which uses FFPE tissue DNA as the sample input. Overall survival (OS) and objective response rate (ORR) by RECIST v1.1 were the primary efficacy endpoints.

This study evaluated the clinical validity of FoundationOne Liquid CDx as a CDx to identify *BRAF* V600E

positive patients from the BEACON clinical trial. FoundationOne Liquid CDx testing was performed on patients with available plasma samples from the BEACON clinical trial that tested positive for *BRAF* V600E by CTA+. Additionally, commercially procured *BRAF* V600E negative CRC patient tissue samples with matched plasma were tested.

The concordance between the CTA and FoundationOne Liquid CDx was evaluated by the PPA and NPA (**Table 66**). The prevalence-adjusted PPV and NPV were also calculated by adjusting for the prevalence of *BRAF* V600E among the intention-to-treat (ITT) population, with 10% and 15% as the estimated prevalence. The PPA, NPA, PPV, NPV, and their two-sided 95% CIs are provided in **Table 67**.

Table 66. Concordance for BRAF V600E between FoundationOne Liquid CDx and the CTA

		CTAs		
		Detected	Not Detected	Total
F1LCDx	Detected	286	3	289
	Not Detected	42	102	144
	Unevaluable	74	16	90
	Total	402	121	523
Agreement Statistics Excluding CDx- Unevaluable Results		PPA: 87.2% (286/328) 95% CI ¹ : (83.1%, 90.4%)	NPA: 97.1% (102/105) 95% CI ¹ : (91.9%, 99.0%)	
Percent Unevaluable		18.4% (74/402)	13.2% (16/121)	

¹Calculated with Wilson 2-sided 95% CI.

Table 67. Concordance Analysis Results

	Prevalence	Numerator	Denominator	Point Estimate (%)	95% Two-Sided CI* (%)
PPA	N/A	286	328	87.20	[83.14, 90.39]
NPA	N/A	102	105	97.14	[91.93, 99.02]
Adjusted PPV	10%	N/A	N/A	77.23	[59.41, 100.00]
Adjusted NPV	10%	N/A	N/A	98.56	[98.17, 98.94]
Adjusted PPV	15%	N/A	N/A	84.34	[69.92, 100.00]
Adjusted NPV	15%	N/A	N/A	97.73	[97.12, 98.33]

*CI was calculated using the Wilson-score method for PPA and NPA, while using the bootstrap method for the adjusted PPV and NPV.

The clinical validity of FoundationOne Liquid CDx was demonstrated by assessing clinical efficacy in the FoundationOne Liquid CDx *BRAF* V600E positive population based on the ORR difference between the Doublet Arm and Control Arm, as well as the log hazard ratio (log(HR)) between the 2 arms from the Cox regression model. The ORR is defined as the proportion of patients with objective response of either confirmed CR or PR based on RECIST V1.1. The ORR for the Doublet Arm and Control Arm as well as the ORR difference are reported in **Table 68** for the following subpopulations: CTA+, F1LCDx+|CTA+, F1LCDx-|CTA+, and FoundationOne Liquid CDx unevaluable|CTA+. **Table 68** also summarizes the median OS by the Kaplan-Meier method for each arm as well as the log(HR) with 95% two-sided CI for each of the aforementioned subpopulations.

Table 68. Primary Efficacy in the Bridging Study Subpopulations

	CTA+	F1LCDx+ CTA+	F1LCDx- CTA+	F1LCDx unevaluable CTA+
# Total	402	286	42	74
ORR for Doublet Arm	19.90%	18.49%	17.39%	28.13%

	CTA+	F1LCDx+ CTA+	F1LCDx- CTA+	F1LCDx unevaluable CTA+
ORR for Control Arm	1.49%	1.43%	0.00%	2.38%
ORR Difference (95% two-sided CI)*	18.41% [12.74%, 24.55%]	17.06% [10.51%, 24.22%]	17.39% [-2.39%, 37.14%]	25.74% [9.73%, 43.10%]
Median OS (months) for Doublet Arm	9.49	7.62	NA [§]	18.89
Median OS (months) for Control Arm	5.88	5.38	12.16	7.16
log(HR) (95% two-sided CI)	-0.51 [-0.76, -0.26]	-0.47 [-0.75, -0.19]	-2.72 [-4.71, -0.74]	-0.44 [-1.23, 0.34]

*CI was calculated using the Newcombe method.

[§]The estimated median OS is NA due to the small number of events in this group (3 events).

The clinical validity of FoundationOne Liquid CDx was demonstrated by estimating the ORR difference and log(HR) between the Doublet Arm and Control Arm. The estimated efficacy results for the FoundationOne Liquid CDx-positive (F1LCDx+) population are shown in **Table 69** below. Estimated efficacy results for the F1LCDx+ population, which were comparable to that in the CTA+ population are shown in **Table 68** above.

Table 69. Estimated Efficacy for the F1LCDx+ Population

	Estimated F1LCDx+ Efficacy with 95% CI (log (HR))	Estimated F1LCDx+ Efficacy with 95% CI (ORR difference)
prev = 10%		
c*=0%	-0.36 [-0.61, -0.12]	13.18 [6.86, 19.50]
c=30%	-0.40 [-0.63, -0.16]	14.34 [8.48, 20.21]
c=50%	-0.42 [-0.65, -0.18]	15.12 [9.48, 20.76]
c=70%	-0.44 [-0.67, -0.21]	15.90 [10.42, 21.38]
c=100%	-0.47 [-0.70, -0.24]	17.06 [11.67, 22.46]
prev = 15%		
c*=0%	-0.40 [-0.65, -0.15]	14.39 [8.20, 20.58]
c=30%	-0.42 [-0.67, -0.17]	15.19 [9.25, 21.14]
c=50%	-0.43 [-0.68, -0.19]	15.73 [9.90, 21.55]
c=70%	-0.45 [-0.69, -0.21]	16.26 [10.52, 22.01]
c=100%	-0.47 [-0.71, -0.23]	17.06 [11.37, 22.76]

*c is the ratio of efficacy between F1LCDx+|CTA- and F1LCDx+|CTA+ populations.

A sensitivity analysis was performed to assess the robustness of the concordance and efficacy results subject to the missing FoundationOne Liquid CDx test results. FoundationOne Liquid CDx *BRAF* V600E status were predicted for the FoundationOne Liquid CDx unevaluable patients (patients with missing or invalid FoundationOne Liquid CDx test results). The concordance analysis and the clinical efficacy were updated by accounting for the imputed data.

The PPA and prevalence adjusted PPV estimates were computed for each of the 50 imputed complete data sets and the summary statistics are shown in **Table 70**.

Table 70. Summary Statistics of PPA and PPV on Imputed Complete Data

	Prev	Min	Q1	Median	Mean	Q3	Max	2.5%	97.5%
PPA (%)	N/A	84.29	85.04	85.54	85.46	85.79	86.78	84.54	86.53
PPV (%)	10%	76.62	76.78	76.89	76.87	76.94	77.14	76.68	77.09
PPV (%)	15%	83.89	84.01	84.08	84.07	84.12	84.28	83.93	84.24

In addition, the drug efficacy for the F1LCDx+|CTA+ population with the imputed complete data set is

shown in **Table 71**. The estimated efficacy results for the F1LCDx+ population in the sensitivity analysis are shown in **Table 72**. The sensitivity analysis demonstrated the robustness of the concordance between CTA and FoundationOne Liquid CDx and drug efficacy estimated in the F1LCDx+ population by accounting for the missingness of FoundationOne Liquid CDx status. This study demonstrated the clinical validity of using FoundationOne Liquid CDx as a CDx device to select metastatic CRC patients with *BRAF* V600E for the treatment with encorafenib in combination with cetuximab.

Table 71. Summary Statistics of Estimated log(HR) and ORR Difference for the F1LCDx+|CTA+ Population on Imputed Complete Data

F1LCDx+ CTA+	Min	Q1	Median	Mean	Q3	Max	2.5%	97.5%
log (HR)	-0.59	-0.55	-0.53	-0.53	-0.51	-0.47	-0.59	-0.48
ORR (%) Difference	17.88	18.61	18.96	18.91	19.28	19.82	17.92	19.72

Table 72. Estimated Efficacy for the F1LCDx+ Population in the Sensitivity Analysis

	Estimated F1LCDx+ Efficacy with 95% CI (log (HR))	Estimated F1LCDx+ Efficacy with 95% CI (ORR difference)
prev = 10%		
c*=0%	-0.41 [-0.66, -0.15]	14.54 [8.27, 20.81]
c=30%	-0.44 [-0.71, -0.18]	15.85 [9.81, 21.89]
c=50%	-0.47 [-0.74, -0.20]	16.73 [10.71, 22.74]
c=70%	-0.49 [-0.77, -0.22]	17.60 [11.50, 23.70]
c=100%	-0.53 [-0.82, -0.24]	18.91 [12.49, 25.34]
prev = 15%		
c*=0%	-0.45 [-0.71, -0.18]	15.90 [9.78, 22.02]
c=30%	-0.47 [-0.74, -0.20]	16.81 [10.75, 22.86]
c=50%	-0.49 [-0.76, -0.21]	17.41 [11.32, 23.50]
c=70%	-0.50 [-0.79, -0.22]	18.01 [11.83, 24.19]
c=100%	-0.53 [-0.82, -0.24]	18.91 [12.49, 25.34]

*c is the ratio of efficacy between F1LCDx+|CTA- and F1LCDx+|CTA+ populations.

10.10 Clinical Bridging Study: Detection of *BRAF* V600E to Determine Eligibility for Treatment with encorafenib in combination with binimetinib

The clinical performance of FoundationOne Liquid CDx for the detection of *BRAF* V600E in plasma samples from patients with NSCLC for treatment with BRAFTOVI® (encorafenib) in combination with MEKTOVI® (binimetinib) was established through a clinical bridging study. All available baseline plasma samples for patients enrolled in the PHAROS (ARRAY-818-202) clinical trial were tested by FoundationOne Liquid CDx in the bridging study. The study results demonstrate concordance between the CTAs and the FoundationOne Liquid CDx assay and establishes the clinical effectiveness of the FoundationOne Liquid CDx assay in selecting *BRAF* V600E positive patients with NSCLC for the treatment with encorafenib in combination with binimetinib.

The PHAROS trial is an open-label, multicenter, single-arm study in patients with *BRAF* V600E-positive metastatic NSCLC. Eligible patients were either treatment-naïve or had received treatment with chemotherapy and/or immunotherapy (previously treated).

The efficacy population for the supplemental new drug applications included 59 treatment-naïve patients, and 39 previously treated patients with the locally confirmed *BRAF* V600E who were enrolled into the PHAROS clinical trial. The clinical trial evaluated the efficacy of encorafenib + binimetinib by screening and enrolling NSCLC patients whose tumors harbored a *BRAF* V600E substitution using either a PCR or NGS-based local laboratory assay and using either tumor tissue or blood.

This study evaluated the clinical validity of FoundationOne Liquid CDx as a CDx to identify *BRAF* V600E positive patients from the PHAROS clinical trial. FoundationOne Liquid CDx testing was performed on patients with available plasma samples from the PHAROS clinical trial that tested positive for *BRAF* V600E by CTA+. Additionally, commercially procured *BRAF* V600E negative NSCLC patient tissue samples with matched plasma were tested.

Table 73. FoundationOne Liquid CDx Bridging Study Sample Accountability

Source of Samples	Total # of Patients	# of Failed or Unavailable for F1LCDx Testing	Total # of F1LCDx Evaluable
CTA+*	98	17	81
CTA- Procured Samples Tested by Cobas PCR assay	28	9	19
CTA- Procured Samples Tested by UW OncoPlex	42	12	30
CTA- from Foundation Medicine Archived Samples	50	0	50
Total	218 (100%)	38 (17.43%)	180 (82.56%)

*Six (6) patients from the clinical trial were enrolled by FoundationOne CDx, and were treated as CTA+.

The PPA was 59.26% (48/81) with two-sided 95% confidence interval (CI) (48.38%, 69.30%) and the NPA was 100% (99/99) with two-sided 95% CI (96.26%, 100%) after excluding FoundationOne Liquid CDx-unevaluable results when considering both patients that were treatment naïve and previously treated (**Table 74**). Since patients were enrolled and initially tested by local CTAs, the prevalence-adjusted PPVs and NPVs were calculated using the PPA and NPA, after adjusting for the prevalence of *BRAF* V600E among the ITT population. In the analysis with 1% prevalence, FoundationOne Liquid CDx demonstrated an adjusted PPV of 100% with two-sided 95% CI (92.59%, 100%) and NPV of 99.59% with two-sided 95% CI (99.48%, 99.69%). PPAs of 62% (31/50) and 55% (17/31) were observed for patients that were from treatment-naïve and previously treated patient cohorts, respectively, indicating comparable detection of the *BRAF* V600E substitution in plasma by FoundationOne Liquid CDx among the two patient populations.

Table 74. Concordance for *BRAF* V600E between FoundationOne Liquid CDx and the CTAs

		CTAs		
		Detected	Not Detected	Total
F1LCDx	Detected	48	0	48
	Not Detected	33	99	132
	Unevaluable	17	21	35
	Total	98	120	218
Agreement Statistics Excluding CDx- Unevaluable Results		PPA: 59.26% (48/81) 95% CI ¹ : (48.38%, 69.30%)	NPA: 100% (99/99) 95% CI ¹ : (96.26%, 100%)	
Percent Unevaluable		17.3% (17/98)	17.5% (21/120)	

¹Calculated with Wilson 2-sided 95% CI.

The clinical validity of FoundationOne Liquid CDx was demonstrated by assessing clinical efficacy in the FoundationOne Liquid CDx *BRAF* V600E positive population based on ORR as the primary efficacy endpoint, which is defined as the proportion of patients with best overall response of confirmed CR or PR as determined by independent review committee (IRC) per RECIST v1.1. To evaluate the

secondary efficacy endpoint, duration of response (DOR), the median of DOR was calculated by the Kaplan-Meier method along with its two-sided 95% CI for all the 98 CTA+ patients. The results are reported in **Table 75** and **Table 76**. The estimated ORR and the corresponding 95% confidence intervals for the F1LCDx+ population in the treatment-naïve cohort and previously treated cohort were 74.19% (58.79%, 89.60%) and 35.29% (12.58%, 58.01%), respectively, which were comparable with the observed ORR for CTA biomarker positive population.

Table 75. Primary Efficacy in the Bridging Study Subpopulations (treatment-naïve Cohort)

	CTA+	F1LCDx+ CTA+	F1LCDx- CTA+	F1LCDx unevaluable CTA+
No. of patients	59	31	19	9
No. of events (CR or PR)	44	23	13	8
ORR (%)	74.58	74.19	68.42	88.89
Two-sided 95% CI for ORR [£]	[62.20, 83.94]	[56.75, 86.30]	[46.01, 84.64]	NA*
Median DOR (Two-sided 95% CI)	N/A** [23.1, N/A [§]]	23.1 [12.0, N/A [§]]	N/A** [N/A [§] , N/A [§]]	16.13 N/A*
# Patients with DOR ≥6 months (%)	33 (75)	15 (65.2)	12 (92.3)	6 (75)
# Patients with DOR ≥12 months (%)	26 (59.1)	11 (47.8)	11 (84.6)	4 (50)

*CI was not calculated since the sample size is less than 10.

[£]CI was calculated using the Wilson-Score method. Please refer to the drug label for the CI calculated using the exact method.

**Median DOR is unavailable since the response rate did not fall below 50% in the Kaplan-Meier estimate.

[§]NAs in the lower (upper) 95% CI of median DOR are due to the lower (upper) 95% CI of the response rate that did not fall below 50%.

Table 76. Primary Efficacy in the Bridging Study Subpopulations (previously treated Cohort)

	CTA+	F1LCDx+ CTA+	F1LCDx- CTA+	F1LCDx unevaluable CTA+
No. of patients	39	17	14	8
No. of events (CR or PR)	18	6	6	6
ORR (%)	46.15	35.29	42.86	75.00
Two-sided 95% CI for ORR [£]	[31.57, 61.42]	[17.31, 58.70]	[21.38, 67.41]	NA*
Median DOR (Two-sided 95% CI)	16.72 [11.93, N/A [§]]	16.72 N/A*	11.93 N/A*	N/A** N/A*
# Patients with DOR ≥6 months (%)	12 (66.7)	5 (83.3)	4 (66.7)	3 (50.0)
# Patients with DOR ≥12 months (%)	6 (33.3)	2 (33.3)	2 (33.3)	2 (33.3)

*CI was not calculated since the sample size is less than 10.

[£]CI was calculated using the Wilson-Score method. Please refer to the drug label for the CI calculated using the Exact method.

**Median DOR is unavailable since the response rate did not fall below 50% in the Kaplan-Meier estimate.

[§]NAs in the upper 95% CI of median DOR are due to the upper 95% CI of the response rate that did not fall below 50%.

To assess the robustness of the data subject to missing FoundationOne Liquid CDx test results, a sensitivity analysis was performed, and multiple imputations were used to impute the FoundationOne Liquid CDx *BRAF* V600E status in the FoundationOne Liquid CDx unevaluable population. The concordance analysis and the clinical efficacy for FoundationOne Liquid CDx *BRAF* V600E positive patients were updated by accounting for the imputed data. Multiple imputations were conducted in the original dataset and a total of 200 imputation data sets were generated. The sensitivity analysis demonstrated the robustness of the clinical bridging results. In the sensitivity analysis, the mean PPA between the CTAs and the FoundationOne Liquid CDx was 61.2% with two-sided 95% empirical

confidence interval [57.73%, 63.92%], which was comparable to the observed data 59.26% with two-sided 95% confidence interval [48.38%, 69.30%]. The adjusted PPV on the imputed complete data was 100% across all prevalence values.

The primary efficacy outcome (ORR) was also estimated for each of the imputed complete datasets. The mean ORR for the F1LCDx+ was estimated to be 76.32% with two-sided 95% confidence interval [62.40%, 90.25%] for treatment naïve patients, and 43.28% with two-sided 95% confidence interval [22.31%, 64.2%] for previously treated patients, respectively. The efficacy results for F1LCDx+ population in the sensitivity analysis are comparable to that of the CTA+ population, which demonstrates the clinical validity of FoundationOne Liquid CDx in identifying *BRAF* V600E positive patients with NSCLC for treatment with encorafenib in combination with binimetinib. The sensitivity analysis also demonstrated the robustness of the concordance and efficacy results to the missing FoundationOne Liquid CDx results.

10.11 Clinical Bridging Study: Detection of *BRCA1* and *BRCA2* Alterations to Determine Eligibility for Treatment with niraparib + abiraterone acetate

The clinical performance of FoundationOne Liquid CDx in detecting *BRCA1*, *BRCA2* alterations (*BRCA1/2*) in patients with prostate cancer (PC) who may benefit from treatment with niraparib in combination with abiraterone acetate and prednisone (AAP) (i.e., AKEEGA plus prednisone) was established via a clinical bridging study. All available baseline plasma samples for patients enrolled in the MAGNITUDE clinical trial were tested by FoundationOne Liquid CDx.

The efficacy of AKEEGA (niraparib and abiraterone acetate) was investigated in Cohort 1 of MAGNITUDE (NCT03748641). The MAGNITUDE study was a Phase 3, randomized, double-blinded, placebo-controlled, multicenter study of AKEEGA versus placebo for treatment of patients with metastatic PC. All patients received prednisone. Participants in the MAGNITUDE study were assigned to cohorts based on homologous recombination repair (HRR) alteration status as determined by tissue (majority F1CDx) and/or plasma CTAs. Cohort 1 includes patients with an HRR gene alteration as detected (i.e., HRR+) by at least one assay (tissue or plasma), and Cohort 2 includes patients where no HRR gene alteration was detected (i.e., HRR-) in both assays or HRR- by one assay and unevaluable by the other.

The clinical validity of FoundationOne Liquid CDx was demonstrated by assessing clinical efficacy in the FoundationOne Liquid CDx *BRCA1/2* positive population based on radiographic progression free survival (rPFS) determined by blinded independent central radiology (BICR) review.

Sample accountability

The clinical bridging analysis population included 473 patients from the MAGNITUDE clinical trial, including all patients from Cohort 1 (n=423) and 50 patients randomly selected from Cohort 2. Both Cohort 1 and Cohort 2 patients were used to support concordance analysis while only Cohort 1 samples were used for the efficacy analysis. Among the 473 samples, 443 were tested by FoundationOne Liquid CDx, 396 yielded valid FoundationOne Liquid CDx testing results and 47 failed lab processing (LC, HC, and sequencing) or post-sequencing QC metrics. The overall success rate is 89.39% (396/443, 95% CI: [86.18%, 91.93%]).

Among the 473 patients enrolled into Cohort 1 and Cohort 2, 225 (47.57%) were *BRCA1/2*+ by the enrolling CTA (i.e., CTA+) and 183 passed F1LCDx testing; 248 (52.43%) were *BRCA1/2*- by the enrolling CTA (i.e., CTA-) and 213 passed F1LCDx testing.

Table 77. Sample Accountability for FoundationOne Liquid CDx vs Enrolling CTA

Enrolling CTA Status	F1LCDx Testing Status	COHORT	N (%)
	Available for F1LCDx testing		202 (42.71%)

Enrolling CTA Status	F1LCDx Testing Status	COHORT	N (%)
CTA+	Passed F1LCDx Testing	COHORT 1	183 (38.69%)
	Failed F1LCDx Testing		19 (4.02%)
	Not Tested by F1LCDx, Not Enough Plasma		8 (1.69%)
	Not Tested by F1LCDx, plasma CTA Unevaluable		15 (3.17%)
	Total		225 (47.57%)
CTA-	Available for F1LCDx testing	COHORT 1	191 (40.38%)
		COHORT 2	50 (10.57%)
	Passed F1LCDx Testing	COHORT 1	169 (35.73%)
		COHORT 2	44 (9.30%)
	Failed F1LCDx Testing	COHORT 1	22 (4.65%)
		COHORT 2	6 (1.27%)
	Not Tested by F1LCDx, Not Enough Plasma	COHORT 1	3 (0.63%)
	Not Tested by F1LCDx, plasma CTA Unevaluable	COHORT 1	4 (0.85%)
Total			248 (52.43%)
Total			473 (100.00%)

The concordance analysis between FoundationOne Liquid CDx and enrolling CTA was performed using samples from both Cohort 1 and Cohort 2. The PPA and NPA were calculated and presented in **Table 78**. Adjusted PPV and NPV were calculated using a prevalence of 9.4% (280/2982), which is the proportion of the *BRCA1/2+* population identified by enrolling CTA from the screening population. The PPV and NPV were estimated as

- Adjusted PPV: 64.09% (95% CI: [51.90%, 80.64%])
- Adjusted NPV: 97.13% (95% CI: [96.46%, 97.78%])

Table 78. Concordance for BRCA1, BRCA2 alterations between FoundationOne Liquid CDx and the Enrolling CTA

		CTA		
		Detected	Not Detected	Total
F1LCDx	Detected	133	9	142
	Not Detected	50	204	254
	Unevaluable	42	35	77
	Total	225	248	473
Agreement Statistics Excluding CDx-Unevaluable Results		PPA: 72.68% (133/183) 95% CI ¹ : (65.80%, 78.62%)	NPA: 95.77% (204/213) 95% CI ¹ : (92.17%, 97.76%)	
Percent Unevaluable		18.67% (42/225)	14.11% (35/248)	

¹Calculated with Wilson 2-sided 95% CI.

A summary of the median rPFS and hazard ratio (HR) was provided in **Table 79** for each subgroup within Cohort 1. For the F1LCDx+|enrolling CTA+ subgroup the estimated HR using a stratified Cox regression was 0.49 (95% CI: [0.29, 0.81]), which suggested a 51% reduction in the risk of radiographic progression when using AKEEGA compared with placebo, comparable with the HR of 0.53 (95% CI: [0.36, 0.79]) for the CTA+ population

Table 79. Estimation of median rPFS and HR

Subgroup	No. of Patients		No. of Events		Median rPFS (months) [95% CI] ¹		HR [95% CI]
	AKEEGA	Placebo	AKEEGA	Placebo	AKEEGA	Placebo	
CTA+	113	112	45	64	16.56 [14.42, NA]	10.87 [8.34, 13.93]	0.53 [0.36, 0.79]
F1LCDx+ CTA+	63	70	25	42	18.43 [13.83, NA]	11.04 [8.31, 16.39]	0.49 [0.29, 0.81]
F1LCDx- CTA+	30	20	12	11	16.66 [14.98, NA]	8.44 [8.28, NA]	0.49 [0.19, 1.26]

Subgroup	No. of Patients		No. of Events		Median rPFS (months) [95% CI] ¹		HR [95% CI]
	AKEEGA	Placebo	AKEEGA	Placebo	AKEEGA	Placebo	
F1LCDx-evaluable CTA+	93	90	37	53	16.66 [14.98, NA]	9.03 [8.31, 13.93]	0.53 [0.34, 0.81]
F1LCDx-unevaluable CTA+	20	22	8	11	13.86 [11.10, NA]	10.91 [7.59, NA]	0.52 [0.18, 1.48]

¹The 95% CI upper/lower bound was NA when the upper/lower bound of the confidence band for rPFS probability did not drop below 50% and thus could not be estimated.

Among the 50 F1LCDx-|CTA+ patients, 23 were plasma CTA+ only (13 F1CDx- and 10 F1CDx unevaluable), 23 were F1CDx+ only (all plasma CTA-), 2 were F1CDx+ and plasma CTA+, and 2 were CTA+ by a local tissue-based test (all F1CDx unevaluable and plasma CTA-). The 25 F1LCDx-|F1CDx+ included 15 *BRCA1/2* homozygous deletions (HD), 2 rearrangements (RE), and 8 short variants (SVs). A total of 33 patients enrolled and treated in MAGNITUDE had a homozygous deletion in *BRCA1/2* as detected by F1CDx; 7 of them were F1LCDx unevaluable, 21 were F1LCDx HD-, and 5 were F1LCDx HD+. The HR estimated by the stratified Cox regression was 0.233 (95% CI: [0.0044, 1.23]) in the F1LCDx-|F1CDx+ HD subpopulation. These results indicate that F1LCDx may miss a subset of patients with prostate cancer harboring *BRCA1/2* homozygous deletions who may derive benefit from AKEEGA since the data demonstrated that the FoundationOne Liquid CDx test did not detect approximately 81% of prostate cancer patients with *BRCA1/2* homozygous deletions who responded to AKEEGA therapy.

Since insufficient samples were observed in the F1LCDx+|CTA- subgroup and the prevalence-adjusted PPV was <100%, the efficacy of the F1LCDx+|CTA- population was estimated using the tipping point method where *c* is a constant that varies from 0% (worst-case scenario) to 100% (best-case scenario) to assess if the estimates of the efficacy for the F1LCDx positive population in cohort 1 are robust under different values of *c*. The HR estimated by the stratified Cox regression ranged between 0.49 (95% CI: [0.33, 0.71]) and 0.63 (95% CI: [0.42, 0.93]) as the scaling factor *c* went from 100% to 0% which demonstrated statistically significant clinical efficacy among the FoundationOne Liquid CDx *BRCA1/2*+ population (**Table 80**).

Table 80. Estimations of HR for the F1LCDx *BRCA1/2*+ population

<i>c</i> ¹	HR between treatment and control arms	95% CI for HR between treatment and control arms
0%	0.63	[0.42, 0.93]
30%	0.58	[0.40, 0.86]
50%	0.55	[0.38, 0.81]
70%	0.53	[0.36, 0.77]
100%	0.49	[0.33, 0.71]

¹ *c* is a constant ranging from 0% to 100% and is used in the tipping point method for efficacy estimation of the F1LCDx+|CTA- population.

A sensitivity analysis was performed to assess the robustness of concordance and efficacy results subject to missing F1LCDx results. Multiple imputation methodology was used to impute the FoundationOne Liquid CDx *BRCA1/2* status for the F1LCDx-unevaluable but CTA-evaluable patients. The concordance and efficacy were re-estimated using the complete dataset including the imputed status. The median of the PPAs calculated using the complete datasets was 73.78% (95% CI: [72.44%, 76.00%]); the median of the prevalence-adjusted PPV was 63.45% (95% CI: [59.55%, 68.45%]); the HR estimated using the complete datasets ranged between 0.49 (95% CI: [0.30, 0.81]) and 0.63 (95% CI: [0.44, 0.91]). A separate sensitivity analysis using the weighted efficacy that considered the efficacy in Cohort 2 as missing was conducted. Following this approach, the HR estimated based on the stratified Cox regression using the complete dataset ranged from 0.49 (95% CI: [0.34, 0.71]) and 0.69 (95% CI: [0.49, 0.96]). Comparable results were seen with those from the observed dataset, which demonstrated that the concordance and efficacy results were robust after accounting for the missing FoundationOne Liquid CDx results.

In summary, this study demonstrated the clinical validity of using FoundationOne Liquid CDx as a CDx device to select patients with PC with *BRCA1*, *BRCA2* alterations for treatment with AKEEGA.

10.12 FoundationOne Liquid CDx Clinical Efficacy Study: Detection of *BRCA1* and *BRCA2* Alterations to Determine Eligibility for Treatment with LYNPARZA® in combination with abiraterone

The clinical performance of FoundationOne Liquid CDx in detecting *BRCA1* and *BRCA2* alterations (*BRCA1/2*) in patients with metastatic castration-resistant prostate cancer who may benefit from LYNPARZA® (olaparib) in combination with abiraterone was established with clinical data generated from FoundationOne Liquid CDx in the clinical study D081SC00001 (hereafter referred to as PROpel).

The PROpel trial was a randomized, double-blind, placebo-controlled, multicenter study of olaparib plus abiraterone relative to placebo plus abiraterone as first line therapy in men with mCRPC. Patients were randomized 1:1 to receive either olaparib plus abiraterone or placebo plus abiraterone. All patients received either prednisone or prednisolone 5 mg twice daily, and a GnRH analog or prior bilateral orchiectomy. Enrollment into the PROpel trial followed an all-comer approach. Genomic testing was conducted after patient randomization and before the primary analysis of the study.

The major efficacy outcome measure of the PROpel study was investigator-assessed radiographic progression free survival (rPFS). Overall survival (OS) was an additional efficacy outcome measure. *BRCA1/2* mutation (*BRCAm*) status was assessed after randomization and before the primary analyses by both NGS-based tumor tissue (FoundationOne CDx) and ctDNA (FoundationOne Liquid CDx) tests.

A total of 1103 patients were enrolled in PROpel. Of these, 796 patients were randomized in PROpel while 307 patients were not randomized. Of the 796 patients randomized in PROpel, tissue samples were available for 782 patients (98.2%; 782/796) to enable FoundationOne CDx testing, and ctDNA samples were available for 794 patients (99.7%; 794/796) to enable FoundationOne Liquid CDx testing.

The concordance between FoundationOne CDx (as reference) and FoundationOne Liquid CDx was evaluated by calculation of the positive percent agreement (PPA), negative percent agreement (NPA), positive predictive value (PPV) and negative predictive value (NPV) in the 491 patients randomized in PROpel with valid results for both FoundationOne CDx and FoundationOne Liquid CDx tests (**Table 81**).

Table 81. Concordance between FoundationOne CDx and FoundationOne Liquid CDx *BRCAm* status in PROpel

		FoundationOne CDx tissue test		
		<i>BRCAm</i>	Non- <i>BRCAm</i>	Total
FoundationOne Liquid CDx ctDNA test	<i>BRCAm</i> ^a	34	18	52
	Non- <i>BRCAm</i> ^b	12	427	439
	Total	46	445	491
	PPA % (95% CI)	73.9 (59.7, 84.4)		
	NPA % (95% CI)	96.0 (93.7, 97.4)		
	PPV % (95% CI)	65.4 (51.8, 76.8)		

	NPV % (95% CI)	97.3 (95.3, 98.4)
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Note: The reference is the tumor tissue test (FoundationOne CDx).

^a Defined as any deleterious or suspected deleterious *BRCA1/2* gene mutation detected.

^b Defined as no deleterious or suspected deleterious *BRCA1/2* gene mutation detected. Test failed/samples are not included in concordance analysis.

PPA = Positive Percentage Agreement, NPA = Negative Percentage Agreement, PPV = Positive Predictive Value, NPV = Negative Predicted Value. The 95% confidence interval (CI) for PPA, NPA, PPV and NPV is calculated using the Wilson method.

The 12 F1LCDx-|F1CDx+ patients included 7 *BRCA1/2* homozygous deletions (HD), 3 short variants (SVs), and 2 rearrangements. A total of 10 patients enrolled and treated in PROpel had a homozygous deletion in *BRCA1/2* as detected by FoundationOne CDx, 3 of them were HD+ and 7 were HD- by FoundationOne Liquid CDx testing. All (7/7) of the HD F1CDx+|F1LCDx- had tumor fraction (TF) below the *BRCA2* HD LoD of the FoundationOne Liquid CDx assay. These results indicate that FoundationOne Liquid CDx may miss a subset of patients with prostate cancer harboring *BRCA1/2* homozygous deletions.

The clinical validity of FoundationOne Liquid CDx was demonstrated by assessing clinical efficacy in the *BRCA1/2* positive population based on rPFS and OS. Of the 796 randomized patients in PROpel, 85 had *BRCAM* determined by either a positive ctDNA test or a tumor tissue test. The clinical efficacy was evaluated in terms of rPFS by investigator assessment and OS. The HR was calculated using a Cox proportional hazards model.

A statistically significant improvement in rPFS for Lynparza/abiraterone compared to placebo/abiraterone was observed in the intention to treat (ITT) population. In an exploratory analysis in the subgroup of 711 patients without an identified *BRCAM*, the rPFS hazard ratio was 0.77 (95% CI: 0.63, 0.96) and the OS hazard ratio was 0.92 (95% CI: 0.74, 1.14), indicating that the improvement in the ITT population was primarily attributed to the results seen in the subgroup of patients with *BRCAM*.

In the analysis of *BRCAM* patients as determined by FoundationOne Liquid CDx, the rPFS hazard ratio was 0.18 (95% CI [0.08, 0.36]) and the OS hazard ratio was 0.31 (95% CI [0.15, 0.63]). The magnitude of treatment effect was also numerically greater in comparison to the non-*BRCAM* subgroup (rPFS HR=0.78; 95% CI [0.63, 0.97] and OS HR=0.89; 95% CI [0.72, 1.10]).

Table 82 summarizes the efficacy results in the 85 patients in PROpel with *BRCAM* as determined by either a positive FoundationOne Liquid CDx test and/or a positive FoundationOne CDx test (the total *BRCAM* population) and in the 69 patients with *BRCAM* as determined by FoundationOne Liquid CDx.

Table 82. Efficacy analyses in PROpel

	Total <i>BRCAm</i> population (n=85)		F1LCDx+ <i>BRCAm</i> population (n=69)	
	Lynparza/abiraterone	Placebo/abiraterone	Lynparza/abiraterone	Placebo/abiraterone
	N = 47	N = 38	N = 39	N = 30
Radiological Progression-Free Survival (rPFS) ^a				
Events, n (%)	14 (30)	28 (74)	12 (31)	25 (83)
Median (95% CI), months	NR (NR, NR)	8 (6, 15)	NR (NR, NR)	8 (5, 11)
Hazard ratio (95% CI) ^b	0.24 (0.12, 0.45)		0.18 (0.08, 0.36)	
Overall Survival (OS)				
Events, n (%)	13 (28)	25 (66)	12 (31)	21 (70)
Median (95% CI), months	NR (NR, NR)	23 (18, 34)	NR (NR, NR)	23 (16, 28)
Hazard ratio (95% CI) ^b	0.30 (0.15, 0.59)		0.31 (0.15, 0.63)	

NR: Not reached

^aInvestigator-assessed

^bCalculated using an unstratified univariable Cox proportional hazards model

A sensitivity analysis was performed to assess the robustness of the clinical efficacy estimated after accounting for the F1LCDx-unevaluable (failed FoundationOne Liquid CDx testing or not tested by FoundationOne Liquid CDx) results. Following imputation, the HR estimated for rPFS based on the Cox proportional hazards model using the complete dataset was 0.19 (95% CI: [0.09, 0.39]) and the HR estimated for OS based on the Cox proportional hazards model following imputation was 0.32 (95% CI: [0.16, 0.65]) in the *BRCAm* subgroup of patients as determined by FoundationOne Liquid CDx testing. Comparable results were seen with those from the observed dataset, which demonstrated the efficacy results were robust after accounting for the missing FoundationOne Liquid CDx results.

In summary, the data from this study demonstrated the clinical validity of using the FoundationOne Liquid CDx assay in identifying patients with metastatic castration-resistant prostate cancer with *BRCA1/2* alterations for the treatment with LYNPARZA® (olaparib) in combination with abiraterone.

10.13 FoundationOne Liquid CDx Clinical Efficacy Study: Detection of *PIK3CA* mutations to determine eligibility with ITOVEBI™ (inavolisib) in combination with palbociclib and fulvestrant

The clinical validity of FoundationOne Liquid CDx assay as a companion diagnostic device for identifying *PIK3CA* mutations in locally advanced or metastatic breast cancer patients who may benefit from treatment with inavolisib in combination with palbociclib and fulvestrant was established using clinical data from the INAVO120 clinical trial.

INAVO120 (WO41554/NCT04191499) is a randomized, double-blind, placebo-controlled trial evaluating the efficacy of the triplet combination of inavolisib plus palbociclib and fulvestrant versus placebo plus palbociclib and fulvestrant in patients with *PIK3CA*-mutated, Hormone Receptor-Positive (HR+), HER2-negative (HER2-) locally advanced or metastatic breast cancer, who have not received prior systemic therapy for locally advanced or metastatic disease and whose disease progressed during or within 12 months of completing adjuvant endocrine therapy. *PIK3CA* mutation (*PIK3CAm*) status was prospectively determined in a central laboratory using the FoundationOne Liquid CDx assay on plasma-derived ctDNA or in local laboratories using various validated PCR or NGS assays on tumor tissue or plasma. All patients were required to provide both a freshly collected pre-treatment blood sample and a tumor tissue sample for central evaluation and determination of *PIK3CAm* status.

The major efficacy outcome measure was investigator (INV)-assessed progression-free survival (PFS) per Response Evaluation Criteria in Solid Tumors (RECIST) version 1.1. Additional efficacy outcome measures included overall survival (OS), INV-assessed objective response rate (ORR), and INV-assessed duration of response (DOR).

A total of 325 patients were included in the NDA efficacy population for inavolisib or placebo plus palbociclib and fulvestrant. Of the 325 patients from the INAVO120 NDA population (after excluding 43 patients from China who were not available for F1LCDx testing), 1.4% (4/282) of patients had unevaluable F1LCDx test results and 98.6% (278/282) of patients had evaluable F1LCDx test results, including 95.4% (269/282) that were positive for one or more study-eligible *PIK3CA* mutation(s) by F1LCDx (i.e., F1LCDx-positive) and 3.2% (9/282) with no *PIK3CA* mutation detected (i.e., F1LCDx-negative). One additional F1LCDx-positive patient was excluded from the efficacy analyses due to not ultimately receiving their planned treatment with inavolisib in combination with palbociclib and fulvestrant.

In the efficacy analysis for the NDA population, the median PFS (months) with 95% 2-sided CI for the inavolisib cohort was 15.0 [11.3, 20.5] months, and the median PFS for the placebo cohort was 7.3 [5.6, 9.3] months. The PFS hazard ratio (HR) for inavolisib in combination with palbociclib and fulvestrant vs. placebo in combination with palbociclib and fulvestrant and the associated 2-sided 95% CI was estimated as 0.43 [0.32, 0.59].

The clinical validity of F1LCDx was demonstrated by assessing clinical efficacy in the F1LCDx PIK3CA mutation-positive population based on progression free survival (PFS) as the primary efficacy endpoint. The efficacy analysis dataset consists of PIK3CA mutation(s) positive, HR+, HER2- locally advanced or metastatic breast cancer patients from the NDA efficacy population, enrolled by a local assay or by the central F1LCDx assay, whose tumors (cfDNA) were F1LCDx-positive.

For each treatment arm, Kaplan-Meier curves were used to estimate the time-to-event distributions. The 50th percentile of Kaplan-Meier estimates were used to estimate the median duration of PFS and are reported with a 2-sided 95% CI in **Table 83**. The HR was calculated using a Cox proportional hazards model.

Table 83. Summary of PFS for Each Treatment Group for F1LCDx-positive Population*

*Treatment groups were defined by actual received treatment indicator (TRT01A) for the clinical validation study.

Efficacy Endpoint	Total PIK3CAm population (n=325)		F1LCDx+ PIK3CAm population (n=268)	
	ITOVEBI + Palbociclib + Fulvestrant N=161	Placebo + Palbociclib + Fulvestrant N=164	ITOVEBI + Palbociclib + Fulvestrant N=137	Placebo + Palbociclib + Fulvestrant N=131
Progression-Free Survival^{a,b}				
Patients with event, n (%)	82 (51)	113 (69)	68	92
Median, months (95% CI)	15.0 (11.3, 20.5)	7.3 (5.6, 9.3)	16.6 (13.4, 24.2)	7.3 (5.8, 10.1)
Hazard ratio (95% CI)	0.43 (0.32, 0.59)		0.42 (0.30, 0.59)	

CI = confidence interval.

^a Per RECIST version 1.1.

^b Based on investigator assessment.

Compared to the placebo cohort, in which the median PFS was 7.3 [5.8, 10.1] months, the median PFS for the inavolisib treatment cohort was 16.6 [13.4, 24.2] months. The PFS hazard ratio (HR) for inavolisib in combination with palbociclib and fulvestrant vs. placebo in combination with palbociclib and fulvestrant and the associated 2-sided 95% CI was estimated as 0.42 [0.30, 0.59], which were comparable to that in the total PIK3CA positive population.

A sensitivity analysis was performed to assess the robustness of the clinical efficacy estimated after accounting for the F1LCDx-unevaluable (failed FoundationOne Liquid CDx testing or not tested by FoundationOne Liquid CDx) results. Following imputation, the estimated HR for PFS based on the Cox proportional hazards model using the complete dataset was 0.44 (95%CI: [0.43, 0.44]) in the PIK3CA+ patients as determined by FoundationOne Liquid CDx testing. Comparable results were seen with those from the observed dataset, which demonstrated the efficacy results were robust after accounting for the missing FoundationOne Liquid CDx results.

10.14 Clinical Bridging Study: Detection of MET single nucleotide variants (SNVs) and indels that lead to MET exon 14 skipping to Determine Eligibility for Treatment with tepotinib

The clinical performance of F1LCDx in detecting SNVs and indels that lead to *MET* exon 14 skipping

alterations in patients with advanced or metastatic NSCLC who may benefit from treatment with tepotinib was established through a clinical bridging study with clinical data for patients from the VISION clinical study (NCT02864992) and biomarker data from F1LCDx results.

The VISION clinical trial is a single-arm, open-label, multicenter, non-randomized, multicohort study of *MET* inhibitor, TEPMETKO (tepotinib) in adult patients with advanced or metastatic NSCLC harboring *MET* exon 14 skipping alterations. Identification of *MET*ex14 skipping alterations was prospectively determined using central laboratories employing either a PCR-based or next-generation sequencing-based clinical trial assay using tissue (58%) and/or plasma (65%) samples.

The efficacy population for tepotinib included 69 treatment-naïve patients, and 83 previously treated patients with locally confirmed *MET*ex14 skipping alterations. The bridging study evaluated the clinical validity of F1LCDx as a CDx to identify *MET* exon 14 skipping alteration positive patients with available plasma samples from the VISION trial that tested positive for *MET* exon 14 skipping alteration by the CTAs (CTA+). Additionally, VISION trial enrollment screen-fails that were determined to be negative for *MET* exon 14 skipping alterations by the CTA (CTA-) were tested by F1LCDx.

The concordance between the CTAs and F1LCDx was assessed by positive percent agreement (PPA) and negative percent agreement (NPA). The PPA was 67.20% (84/125) with two-sided 95% confidence interval (CI) [58.56%, 74.81%] and the NPA was 100% (116/116) with two-sided 95% CI [96.79%, 100%] after excluding F1LCDx-unevaluable results when considering both patients that were treatment naïve and previously treated (**Table 84**). Since patients were enrolled and initially tested by local CTAs, the prevalence-adjusted PPVs and NPVs were calculated using the PPA and NPA, after adjusting for the prevalence of *MET* exon 14 skipping alteration among the ITT population (**Table 85**). In the analysis with 3% prevalence, F1LCDx demonstrated an adjusted PPV of 100% with two-sided 95% CI [95.63%, 100%] and NPV of 99.00% with two-sided 95% CI [98.75%, 99.24%].

Table 84. Contingency Table for *MET* exon 14 Status Between CTAs (Tissue and Plasma) and F1LCDx

	CTA		
	CTA+	CTA-	Total
F1LCDx+	84	0	84
F1LCDx-	41	116	157
F1LCDx Unevaluable	27	3	30
Total	152	119	271
Agreement Statistics Excluding CDx- Unevaluable Results	PPA:67.20% (84/125) 95% 2-sided CI ¹ : [58.56, 74.81]	NPA: 100.00% (116/116) 95% 2-sided CI ¹ : [96.79, 100.00]	
Percent Unevaluable	17.8% (27/152)	2.52% (3/119)	

¹Calculated with the Wilson-score method 2-sided 95% CI.

Table 85. Concordance Analysis Results

	Prevalence	Numerator	Denominator	Point Estimate (%)	95% Two-Sided CI* (%)
PPA	N/A	84	125	67.20	[58.56, 74.81]
NPA	N/A	116	116	100.00	[96.79, 100.00]
Adjusted PPV	3%	N/A	N/A	100.00	[95.63, 100.00]
Adjusted NPV	3%	N/A	N/A	99.00	[98.75, 99.24]

*CI was calculated using the Wilson-score method for PPA, NPA, and PPV while using the bootstrap method for NPV .

The clinical validity of F1LCDx was demonstrated by assessing clinical efficacy in the F1LCDx *MET*ex14 positive population based on ORR as the primary efficacy endpoint, which is defined as the proportion of patients with best overall response of confirmed Complete Response (CR) or Partial Response (PR) as determined by Blinded independent review committee (BIRC) per Response Evaluation Criteria in Solid Tumors (RECIST) v1.1. To evaluate the secondary efficacy endpoint, duration of response (DOR), the median DOR was calculated by the Kaplan-Meier method along with its two-sided 95% CI for all the patients. The results are reported in **Table 86** and **Table 87** for treatment-naïve patients and previously treated patients, respectively. Because NPA and PPV are 100%, the point estimate of ORR for F1LCDx+ population was the same as that for CTA+/F1LCDx+ population within the respective cohort by treatment lines. The estimated ORR and the corresponding 95% CIs for the F1LCDx+ population in the treatment-naïve cohort and previously treated cohort were 50.0% [34.10%, 65.90%] and 36.96% [23.01%, 50.91%], respectively, which were comparable with the observed ORR for the CTA+ population in the respective cohort by treatment lines.

Table 86. Efficacy in Treatment-naïve Patients (1L) from NDA Population

	CTA+	F1LCDx+ CTA+	F1LCDx- CTA+	F1LCDx evaluable CTA+	F1LCDx unevaluable CTA+
No. of patients	69	38	21	59	10
No. of events (CR or PR)	30*	19	9	28	2*
ORR (%)	43.48	50.00	42.86	47.46	20.00
95% two-sided CI for ORR (%)	[32.43, 55.21]	[34.85, 65.15]	[24.47, 63.45]	[35.27, 59.96]	[5.67, 50.98]

*One (1) 1L patient determined as a responder by IRC was not considered a responder by the FDA and was treated as a non-responder in the clinical bridging analysis. Note that this patient was F1LCDx unevaluable.

Table 87. Efficacy in Previously Treated Patients (2L+) from NDA Population

	CTA+	F1LCDx+ CTA+	F1LCDx- CTA+	F1LCDx evaluable CTA+	F1LCDx unevaluable CTA+
No. of patients	83	46	20	66	17
No. of events (CR or PR)	36*	17	9*	26*	10
ORR (%)	43.37	36.96	45.00	39.39	58.82
95% two-sided CI for ORR (%)	[33.24, 54.09]	[24.52, 51.40]	[25.82, 65.79]	[28.50, 51.45]	[36.01, 78.39]

*One (1) 2L+ patient determined as a responder by IRC was not considered as a responder by the FDA and was treated as a non-responder in the clinical bridging analysis. Note that this patient was F1LCDx negative.

To assess the robustness of the data subject to missing F1LCDx test results, a sensitivity analysis was performed, and multiple imputations were used to impute the F1LCDx *MET* exon 14 skipping alteration status in the F1LCDx unevaluable population. The concordance analysis was re-conducted based on the imputed data. The PPA estimates based on the imputed complete datasets has a mean of 67.13% with two-sided 95% empirical CI [64.58%, 69.44%], comparable to the PPA calculated using the observed data (i.e., excluding the F1LCDx-unevaluable samples) which was 67.20% with two-sided 95% Wilson-score CI [58.56%, 74.81%]. The adjusted PPV based on the imputed complete datasets was 100% across all imputations.

The clinical efficacy (ORR) were also re-estimated based on the imputed data. The mean ORR for the F1LCDx+ population was 46.00% with two-sided 95% CI [31.14%, 60.86%] for the treatment-naïve patients, and 39.88% with two-sided 95% CI [26.28%, 53.47%] for the previously treated patients,

respectively. The efficacy results after imputation are comparable to those estimated using observed data among treatment-naïve patients and previously treated patients, respectively. In summary, the sensitivity analysis demonstrated the robustness of concordance and efficacy results by accounting for the missing F1LCDx status.

10.15 FoundationOne Liquid CDx Clinical Efficacy Study: Detection of *HRR* gene alterations to determine eligibility for treatment with TALZENNA® (talazoparib) in combination with XTANDI® (enzalutamide)

The clinical effectiveness of F1LCDx for detecting *HRR* gene alterations in mCRPC patients who may benefit from treatment with talazoparib in combination with enzalutamide was demonstrated using clinical data generated from F1LCDx in Part 2 of the TALAPRO-2 clinical study.

The TALAPRO-2 clinical trial is an international, Phase 3, two-part study enrolling patients with mCRPC where no systemic cancer treatments have been initiated after documentation of mCRPC, with the exception of androgen deprivation therapy and first-generation anti-androgen agents. Part 1 was open-label and non-randomized and evaluated the safety, tolerability, and pharmacokinetics (PK) of talazoparib in combination with enzalutamide. Part 2 was randomized, double-blinded, and placebo-controlled and evaluated the safety and efficacy of talazoparib in combination with enzalutamide compared with placebo in combination with enzalutamide. Part 2 of the study included 2 cohorts and randomized patients 1:1 to talazoparib in combination with enzalutamide versus placebo in combination with enzalutamide. The major efficacy outcome measure of Part 2 was radiographic progression-free survival (rPFS) evaluated according to Response Evaluation Criteria in Solid Tumors (RECIST), version 1.1 and Prostate Cancer Working Group (PCWG3) (bone) criteria, assessed by Blinded Independent Central Review (BICR). A secondary efficacy outcome measure was Overall Survival (OS).

The first cohort (Cohort 1) of Part 2 enrolled 805 mCRPC patients unselected for HRR status (referred to as an all-comers population). However, HRR deficiency assessment prior to randomization was required for stratification. After enrollment for Cohort 1 was closed, enrollment into the study continued but was restricted to patients with HRR deficiencies (Cohort 2). Cohort 2 enrolled 230 additional patients harboring *HRR* gene alterations that were likely to sensitize the patient's tumor to poly (adenosine diphosphate [ADP]-ribose) polymerase (PARP) inhibition (HRR-deficient). Patients with alterations in at least one of the 12 *HRR* genes (*ATM*, *ATR*, *BRCA1*, *BRCA2*, *CDK12*, *CHEK2*, *FANCA*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, or *RAD51C*) were identified prior to randomization by central testing of tumor tissue or blood samples (liquid biopsy) using primarily the F1CDx and/or the F1LCDx assays.

The concordance between FoundationOne CDx (as reference) and FoundationOne Liquid CDx was evaluated by calculation of the positive percent agreement (PPA), negative percent agreement (NPA), positive predictive value (PPV) and negative predictive value (NPV) in the 805 patients (i.e., the all-comers population) enrolled in Cohort 1 of Part 2 of the TALAPRO-2 study (**Table 88**) using all available samples [i.e., by prospective (on screening phase samples) and retrospective (on additional samples collected at screening and tested retrospectively) testing results] with valid results .

Table 88. Concordance between FoundationOne CDx and FoundationOne Liquid CDx for HRRm status in Cohort 1 of the TALAPRO-2 study.

		FoundationOne CDx tissue test			
		HRRm	Non-HRRm	Unevaluable	Total
FoundationOne Liquid CDx ctDNA test	HRRm	95	46	53	194
	Non-HRRm	27	297	170	494
	Unevaluable	10	30	77	117
	Total	132	373	300	805
	PPA % (95% CI)			77.87 (69.72, 84.32)	
	NPA % (95% CI)			86.59 (82.57, 89.79)	
	PPV % (95% CI)			67.38 (59.27, 74.56)	
	NPV % (95% CI)			91.67 (88.15, 94.21)	

Of the 805 mCRPC patients enrolled into Cohort 1, 169 patients were HRR-deficient by prospective testing and thus, there were altogether 399 HRR-deficient patients including 230 patients with prospectively assessed HRRm disease subsequently enrolled after Cohort 1 completed enrollment. The clinical validation study was based on the combined HRR-deficient population in the TALAPRO-2 study, i.e. the 399-HRR deficient patients from Cohort 1 and Cohort 2 based on prospective testing results. Of these 399 HRR-deficient patients, a total of 354 patients had valid results by F1LCDx and 45 were not tested or did not have valid results by F1LCDx. Out of the 354 patients with F1LCDx valid results, 287 were HRR+ by F1LCDx and 67 were HRR- by F1LCDx (but positive by other enrolling assays).

The clinical validity of F1LCDx was demonstrated by assessing clinical efficacy in the F1LCDx HRR-deficient (HRRm) positive population based on rPFS (n=287).

The TALAPRO-2 study met its primary endpoint, as treatment with talazoparib in combination with enzalutamide resulted in a clinically meaningful and statistically significant improvement in rPFS in the intent-to-treat (ITT), HRRm population. Please refer to the TALZENNA USPI for rPFS and OS results .

As presented in **Table 89**, the median rPFS in the F1LCDx-HRR deficient population was 22.14 months (95% two-sided CI: [16.59, non-estimable (NE)]) in the experimental treatment group and 11.07 months (95% two-sided CI: [10.91, 16.43]) in the placebo group as estimated by the Kaplan-Meier method. The estimated HR based on stratified Cox regression models and the Breslow tie handling method was 0.48 (95% two-sided CI: [0.34, 0.69]) comparing the treatment group versus the placebo group. The results demonstrate improved rPFS and reduced risk of disease progression or death in patients who received treatment with talazoparib in combination with enzalutamide.

Table 89. Efficacy analyses for F1LCDx HRRm population from both Cohorts 1 and 2 in TALAPRO-2

	ITT Total HRRm population (n=399)*		F1LCDx + HRRm population (n=287)	
	Talazoparib/ enzalutamide N = 200	Placebo/ enzalutamide N = 199	Talazoparib/ enzalutamide N = 142	Placebo/ enzalutamide N = 145
rPFS Events, n (%)	66 (33)	104 (52)	53 (37)	74 (51)
Median rPFS (95% CI), months	NE(21.9, NE)	13.8 (11.0, 16.7)	22.14 (16.59, NE)	11.07 (10.91, 16.43)
Hazard ratio (95% CI) ^a	0.45 (0.33, 0.61)		0.48 (0.34, 0.69)	

NE: non estimable. Median rPFS and the associated CI bounds may be unavailable when the rPFS rate did not fall below 50% in the Kaplan-Meier estimate.

*Combined HRR-deficient population in the TALAPRO-2 study from Cohorts 1 and 2 (169 from Cohort 1 and 230 from Cohort 2) based on prospective testing (i.e., on screening samples) only.

^aCalculated using a stratified univariable Cox proportional hazards model.

A sensitivity analysis was performed to assess the robustness of the clinical efficacy estimated after accounting for the F1LCDx-unevaluable (failed F1LCDx testing or not tested by F1LCDx) results. Following imputation, the HR estimated for rPFS based on the Cox proportional hazards model using the complete dataset was 0.43 (two-sided 95% empirical CI: [0.41, 0.45]) in the HRRm population as determined by F1LCDx testing. Comparable results were seen with those from the observed dataset, which demonstrated the efficacy results were robust after accounting for the missing F1LCDx results.

In addition to the efficacy analysis based on Cohorts 1 and 2 to support the therapeutic approval, to further evaluate the clinical validity of F1LCDx, an additional analysis was conducted in the all-comers population of the TALAPRO-2 study (n=805, Cohort 1). In the F1LCDx HRRm population from Cohort 1 (n=194), the median rPFS was 21.88 months (95% two-sided CI: [16.59, NE]) in the experimental treatment group and 13.77 months (95% two-sided CI: [10.61, 22.47]) in the placebo group. The estimated HR was 0.59 (95% two-sided CI: [0.40, 0.88]) comparing the treatment group versus the placebo group (Table 89). Patients in Cohort 1 of the TALAPRO-2 study without HRR alterations as determined by F1LCDx (n=494) had an estimated rPFS HR=0.72 (95% two-sided CI: [0.54, 0.95]) (Table 90). These results in Cohort 1 further support the clinical validity of F1LCDx for the detection of HRR gene alterations in mCRPC.

Table 90. Additional efficacy analyses for F1LCDx HRRm population in Cohort 1 (all-comers population evaluated prospectively and retrospectively) of the TALAPRO-2

	HRRm population (F1LCDx+) n=194		Non-HRRm population (F1LCDx-) n=494	
	Talazoparib/ enzalutamide N = 94	Placebo/ enzalutamide N = 99	Talazoparib/ enzalutamide N=245	Placebo/ enzalutamide N=245

rPFS Events, n (%)	46 (49)	55 (55)	87 (35)	108 (44)
Median rPFS (95% CI), months	21.88 (16.59, NE)	13.77 (10.61, 22.47)	NE (33.05, NE)	25.13 (21.95, NE)
Hazard ratio (95% CI) ^a	0.59 (0.40, 0.88)		0.72 (0.54, 0.95)	

^aCalculated using a stratified univariable Cox proportional hazards model.

11 CDx Classification Criteria

11.1 CDx classification criteria for ALK rearrangements, qualifying NSCLC patients for therapy with ALECENSA® (alectinib):

- The *ALK* rearrangement must have pathogenic driver status (Foundation Medicine driver status of “known” or “likely”)
- AND the disease type must be NSCLC
- AND one of the following two conditions must hold:
 1. The partner gene is *EML4*, or
 2. The *ALK* breakpoint occurs within *ALK* intron 19

11.2 CDx classification criteria for EGFR alterations, qualifying NSCLC patients for therapy with EGFR Tyrosine Kinase Inhibitors (TKI) approved by FDA:

- Base substitutions resulting in *EGFR* L858R
- In-frame deletions occurring within *EGFR* exon 19

11.3 CDx classification criteria for BRCA1, BRCA2, and ATM alterations, qualifying prostate cancer patients for therapy with LYNPARZA® (olaparib):

Table 91 describes the criteria for classifying *BRCA1*, *BRCA2*, or *ATM* alterations known to be deleterious to protein function.

Table 91. Classification Criteria for BRCA1, BRCA2, and ATM

Genes (Transcript)	Variant class	Biomarker description
ATM (NM_000051) BRCA1 (NM_007294) BRCA2 (NM_000059)	Short variant	Any nonsense ¹ , frameshift, or splice site ² variant • For BRCA2, truncating mutations must occur upstream of bases encoding amino acid 3326 Any of the ATM, BRCA1, or BRCA2 alterations listed in Table 92 , Table 93 , and Table 94 .
	Copy number	Homozygous deletion of one or more exons, regardless of transcript • F1LCDx will only include copy number loss in BRCA1 and BRCA2
	Rearrangement	Any inactivating rearrangement, regardless of transcript

¹ Missense mutations in the start codon (except for those in the appendix tables) and short variant deletions spanning from upstream of the start codon (annotated as M1?) are biomarker negative.

² This rule is limited to splice site variants within the donor or acceptor sites, defined as the first two or last two bases of the intron.

Table 92. List of short variants in ATM NM_000051*

M1I	E2039K	A2622V	F2827C	splice site 331+5G>A
M1L	A2067D	D2625_A2626>EP	R2832C	splice site 8418+5_8418+8delGTGA
M1T	R2227C	V2662D	S2855_V2856>RI	
P292L	Y2470D	D2708N	D2913Y	
D2016G	A2524P	V2716A	R3008C	
R2032K	R2547_S2549del	G2765S	R3008H	

Table 93. List of short variants in BRCA1 NM_007294*

M1I	C47S	T1685A	W1718C	A1823T
M1R	C47Y	T1685I	S1722F	V1833M
M1T	C61Y	H1686R	V1736A	W1837C
M1V	C61G	V1688del	V1736G	W1837G
M18K	C61S	M1689R	G1738E	W1837R
M18T	C64G	T1691I	G1738R	V1838E
L22S	C64R	T1691K	D1739G	Y1853C
C24R	C64Y	D1692Y	D1739V	splice site 212+3A>G
I26N	C64W	D1692H	G1748D	splice site 213-11T>G
T37K	R71G	D1692N	R1753T	splice site 213-12A>G
T37R	R71K	A1693del	K1759N	splice site 302-3C>G
C39R	R71M	C1697R	L1764P	splice site 4675+3A>T
C39Y	R71T	R1699Q	I1766S	splice site 4986+3G>C
C39G	S770L	R1699W	G1770V	splice site 4986+5G>A
C39W	R1495K	L1705P	M1775K	splice site 4986+6T>C
H41R	R1495M	G1706E	M1775R	splice site 4986+6T>G
C44F	R1495T	G1706R	L1780P	splice site 5074+3A>G
C44S	E1559K	A1708E	C1787S	splice site 5194-12G>A
C44Y	E1559Q	V1714G	C1787_G1788>SD	splice site 5406+4A>G
C47F	A1623G	S1715N	G1788V	
C47R	S1655F	S1715R	P1812A	

Table 94. List of short variants in BRCA2 NM_000059*

M1R	K1530N	R2659G	D2723G	D3095E
M1I	R2336H	R2659K	D2723H	D3095G
M1V	R2336P	R2659T	D2723V	N3124I
M1T	R2336L	Y2660D	G1724W	N3187K
D23N	T2412I	E2663K	Y2726C	splice site 316+4delA
D23Y	L2510P	E2663V	G2748D	splice site 316+5G>A
S142I	R1602T	S2670L	R2784W	splice site 8487+3A>G
S142N	H2623R	I2675V	G2793R	splice site 8754+3G>C
V159M	W2626C	L2686P	Q2829R	splice site 8754+4A>G
G173R	W2626R	L2688P	A2911E	splice site 8754+5G>A
V211I	I2627F	T2722K	E3002K	splice site 8954-5A>G
V211L	L2647P	T2722R	R3052W	
Y600C	L2653P	D2723A	G3076V	

**Note: This biomarker definition includes ATM and BRCA1/2 inactivating mutation lists that may change over time as a result of periodic review of new evidence, in accordance with FDA-approved variant classification procedures.*

11.4 CDx classification criteria for BRCA1 and BRCA2 alterations, qualifying prostate cancer patients for therapy with RUBRACA® (rucaparib):

Table 95 describes the criteria for classifying *BRCA1* or *BRCA2* alterations known to be deleterious to protein function.

Table 95. Classification Criteria for BRCA1 and BRCA2

Genes (Transcript)	Variant class	Biomarker description
BRCA1 (NM_007294) BRCA2 (NM_000059)	Short variant	Any nonsense ¹ , frameshift, or splice site ² variant For BRCA2, truncating mutations must occur upstream of bases encoding amino acid 3326 Any of the BRCA1 or BRCA2 alterations listed in Table 93 and Table 94 .
	Copy number	Homozygous deletion of one or more exons, regardless of transcript
	Rearrangement	Any inactivating rearrangement, regardless of transcript

¹ Missense mutations in the start codon (except for those in the appendix tables) and short variant deletions spanning from upstream of the start codon (annotated as M1?) are biomarker negative.

² This rule is limited to splice site variants within the donor or acceptor sites, defined as the first two or last two bases of the intron.

11.5 CDx classification criteria for PIK3CA alterations, qualifying breast cancer patients for therapy with PIQRAY® (alpelisib):

Presence of *PIK3CA* mutation(s): H1047R; E545K; E542K; C420R; E545A; E545D [1635G>T only]; E545G; Q546E; Q546R; H1047L; or H1047Y

11.6 CDx classification criteria for SNVs and Indels that lead to MET exon 14 skipping:

A SNV or indel in *MET* shall be considered to result in skipping of exon 14 if one or more of the following criteria are met:

1. Deletions greater than or equal to 5 bp that affect positions -3 to -30 in the intronic region immediately adjacent to the splice acceptor site at the 5' boundary of *MET* exon 14.
2. Indels affecting positions -1 or -2 at the splice acceptor site of the 5' boundary of *MET* exon 14.
3. Base substitutions and indels affecting positions 0, +1, +2, or +3 at the splice donor site of the 3' boundary of *MET* exon 14.

11.7 CDx classification criteria for NTRK fusions:

Rearrangements in *NTRK1*, *NTRK2*, or *NTRK3* shall be considered CDx biomarker positive, that is, to lead to a *NTRK1*, *NTRK2*, or *NTRK3* RNA fusion, if the following criterion is met:

- In-strand rearrangement events that may lead to an *NTRK1*, *NTRK2* or *NTRK3* RNA fusion with a previously reported or novel partner gene in which the kinase domain is not disrupted. This also includes rearrangement events that result in reciprocal fusions (*NTRK* may be on either the 5' or the 3' end of the detected fusion).

In this regard out-of-strand events are considered as non-fusion rearrangements and are classified as CDx biomarker-negative. Intragenic fusions in which genomic rearrangement events are wholly internal to the *NTRK1*, *NTRK2*, or *NTRK3* genes (i.e., *NTRK1-NTRK1*, *NTRK2-NTRK2*, *NTRK3-NTRK3* events) are also considered biomarker-negative. Unidentified partners (encoded as N/A) or LINC non-coding partners are also considered CDx biomarker-negative.

11.8 CDx classification criteria for *ROS1* fusions

Rearrangements in *ROS1* shall be considered CDx biomarker positive, i.e., to lead to *ROS1* RNA fusion, if the following condition is met:

- In-strand rearrangement events that may lead to a *ROS1* RNA fusion with another protein coding gene in which the *ROS1* kinase domain is not disrupted. *ROS1* must be on the 3' end of the detected fusion.

In this regard, out-of-strand events are considered as non-fusion rearrangements and are classified as CDx biomarker-negative. Intragenic fusions in which genomic rearrangement events are wholly internal to the *ROS1* (i.e., *ROS1-ROS1* events) are also considered biomarker-negative. Unidentified partners (encoded as N/A) or LINC non-coding partners are also considered CDx biomarker-negative. *ROS1* fusions with novel partners are required to be in frame.

11.9 CDx classification criteria for *BRAF* V600E

- Base alterations resulting in *BRAF* V600E

11.10 CDx classification criteria for *BRCA1* and *BRCA2* alterations, qualifying prostate cancer patients for therapy with AKEEGA® (niraparib + abiraterone acetate)

Table 96 describes the criteria for classifying *BRCA1* or *BRCA2* alterations known to be deleterious to protein function.

Table 96. Classification Criteria for *BRCA1* and *BRCA2*

Genes (Transcript)	Variant class	Biomarker description
<i>BRCA1</i> (NM_007294) <i>BRCA2</i> (NM_000059)	Short variant	Any nonsense ¹ , frameshift, or splice site ² variant • For <i>BRCA2</i>, truncating mutations must occur upstream of bases encoding amino acid 3326 Any of the <i>BRCA1</i> or <i>BRCA2</i> alterations listed in Table 93 and Table 94 .
	Copy number	Homozygous deletion of one or more exons, regardless of transcript
	Rearrangement	Any inactivating rearrangement, regardless of transcript

¹ Missense mutations in the start codon (except for those in the appendix tables) and short variant deletions spanning from upstream of the start codon (annotated as M1?) are biomarker negative.

² This rule is limited to splice site variants within the donor or acceptor sites, defined as the first two or last two bases of the intron.

11.11 CDx classification criteria for *BRCA1* and *BRCA2* alterations, qualifying prostate cancer patients for therapy with LYNPARZA® in combination with abiraterone

Table 97 describes the criteria for classifying *BRCA1* or *BRCA2* alterations known to be deleterious to protein function.

Table 97. Classification Criteria for BRCA1 and BRCA2

Genes (Transcript)	Variant class	Biomarker description
BRCA1 (NM_007294) BRCA2 (NM_000059)	Short variant	Any nonsense ¹ , frameshift, or splice site ² variant For BRCA2, truncating mutations must occur upstream of bases encoding amino acid 3326 Any of the BRCA1 or BRCA2 alterations listed in Table 93 and Table 94 .
	Copy number	Homozygous deletion of one or more exons, regardless of transcript
	Rearrangement	Any inactivating rearrangement, regardless of transcript

¹ Missense mutations in the start codon (except for those in the appendix tables) and short variant deletions spanning from upstream of the start codon (annotated as M1?) are biomarker negative.

² This rule is limited to splice site variants within the donor or acceptor sites, defined as the first two or last two bases of the intron.

11.12 CDx classification criteria for PIK3CA alterations, qualifying breast cancer patients for therapy with ITOVEBI™ (inavolisib) in combination with with palbociclib and fulvestrant

Plasma samples meet the biomarker eligibility requirements to assign patients to treatment with inavolisib plus palbociclib and fulvestrant if any of the short variant alterations listed in Table 98 below is detected.

Table 98. List of Eligible PIK3CA Short Variant Alterations

R88Q	N345D	E453G	E542V	Q546H	H1047L	G1049R
G106A	N345H	E453K	E545A	Q546K	H1047N	G1049S
G106D	N345I	E453Q	E545D	Q546L	H1047P	
G106R	N345K	E453V	E545G	Q546P	H1047Q	
G106S	N345S	E542A	E545K	Q546R	H1047R	
G106V	N345T	E542D	E545L	M1043I	H1047T	
K111N	N345Y	E542G	E545Q	M1043T	H1047Y	
K111R	C420R	E542K	E545R	M1043V	G1049A	
K111E	E453A	E542Q	E545V	H1047D	G1049C	
G118D	E453D	E542R	Q546E	H1047I	G1049D	

11.13 CDx classification criteria for HRR gene alterations, qualifying prostate cancer patients for therapy with TALZENNA® (talazoparib) in combination with XTANDI® (enzalutamide).

Table 99 describes the criteria for classifying *HRR* gene alterations known to be deleterious to protein function.

Table 99. Classification Criteria for *HRR* Gene Alterations

Gene (Transcript)	Variant Class	Biomarker Rules
<i>ATM</i> (NM_000051) <i>ATR</i> (NM_001184) <i>BRCA1</i> (NM_007294) <i>BRCA2</i> (NM_000059) <i>CDK12</i> (NM_016507) <i>CHEK2</i> (NM_007194) <i>FANCA</i> (NM_000135) <i>MLH1</i> (NM_000249) <i>MRE11A</i> (NM_005590) <i>NBN</i> (NM_002485) <i>PALB2</i> (NM_024675) <i>RAD51C</i> (NM_058216)	Short Variant	Any nonsense, frameshift, or splice site alteration ¹ - Any splice alterations within the splice donor or acceptor site² - For <i>BRCA2</i>, truncating mutations must occur upstream of bases encoding amino acid 3326 Any of the additional mutations listed in Table 92-Table 94 and Table 100-Table 101 .
	Copy Number	Homozygous deletion of one or more exons, regardless of transcript
	Rearrangement	Any inactivating rearrangement, regardless of transcript

1 Missense mutations in the start codon (except for those in the Appendix 1) and short variant deletions spanning from upstream of the start codon (annotated as M1?) are biomarker negative.

2 This rule is limited to splice site variants within the donor or acceptor sites, defined as the first two or last two bases of the intron.

Table 100. Eligible *CHEK2* Short Variants

R117G	K373E
G151S	A392V

Table 101. Eligible *FANCA*, *MLH1* and *RAD51C* Short Variants

Gene	Short variant
<i>FANCA</i>	F320L, F1263del
<i>MLH1</i>	R265C
<i>RAD51C</i>	L219S

PATIENT

DISEASE Prostate cancer (NOS)
NAME
DATE OF BIRTH
SEX
MEDICAL RECORD #

PHYSICIAN

ORDERING PHYSICIAN
MEDICAL FACILITY
ADDITIONAL RECIPIENT
MEDICAL FACILITY ID
PATHOLOGIST

SPECIMEN

SPECIMEN ID
SPECIMEN TYPE
DATE OF COLLECTION
SPECIMEN RECEIVED

FDA-Approved Content

Companion Diagnostic (CDx) Findings

A companion diagnostic provides essential information for the safe and effective use of a corresponding drug or biological product. This table contains therapies associated with FoundationOne®Liquid CDx's FDA-approved companion diagnostic indications.

GENOMIC FINDINGS
CHEK2 W114* #

CDx-INDICATED THERAPIES
TALZENNA® (talazoparib) in combination with **XTANDI®** (enzalutamide)

Tumor Profiling Results

FoundationOne®Liquid CDx is FDA-approved to provide tumor mutation profiling results for oncology patients with solid tumors.

SHORT VARIANTS AND SELECT REARRANGEMENTS AND COPY NUMBER ALTERATIONS IDENTIFIED

Results reported in this section that are not designated as CDx findings are not prescriptive or conclusive for labeled use of any specific therapeutic product. See *professional services* section for information on the alterations listed in this section as well as any additional detected copy number alterations, gene rearrangements, or biomarkers. Please refer to the appendix for the description of the biomarker levels.

Companion diagnostic (CDx) findings
CHEK2 W114* #

Other biomarkers with potential clinical significance
ATM L2452P #

Variants in this gene may be derived from a nontumor source such as clonal hematopoiesis (CH). The efficacy of targeting such nontumor somatic alterations (e.g., CH) is unknown.

Please refer to appendix for Explanation of Clinical Significance Classification and for variants of unknown significance (VUS).

ORDERED TEST #

APPENDIX

About FoundationOne®Liquid CDx

INTENDED USE

FoundationOne Liquid CDx is a qualitative next generation sequencing based *in vitro* diagnostic test that uses targeted high throughput hybridization-based capture technology to analyze 324 genes and report genomic alterations in 311 genes. These include substitutions, insertions and deletions (indels) in 311 genes, rearrangements in 8 genes and copy number alterations in 3 genes. FoundationOne Liquid CDx utilizes circulating cell-free DNA (cfDNA) isolated from plasma derived from anti-coagulated peripheral whole blood of cancer patients collected in FoundationOne Liquid CDx cfDNA blood collection tubes included in the FoundationOne Liquid CDx Blood Sample Collection Kit. The test is intended to be used as a companion diagnostic to identify patients who may benefit from treatment with the targeted therapies listed in Table 1 in accordance with the approved therapeutic product labeling.

Additionally, FoundationOne Liquid CDx is intended to provide tumor mutation profiling to be used by qualified health care professionals in accordance with professional guidelines in oncology for patients with solid malignant neoplasms.

A negative result from a plasma specimen does not mean that the patient's tumor is negative for genomic findings. Patients with the tumor types above who are negative for the mutations listed in Table 1 (see ** footnote under Table 1 for *NTRK1/2/3* and *ROS1* fusions for ROZLYTREK® and *MET* SNVs and indels that lead to *MET* exon 14 skipping for TEPMETKO®) should be reflexed to routine biopsy and their tumor mutation status confirmed using an FDA-approved tumor tissue test, if feasible.

Genomic findings other than those listed in Table 1 are not prescriptive or conclusive for labeled use of any specific therapeutic product.

TABLE 1: COMPANION DIAGNOSTIC INDICATIONS

TUMOR TYPE	BIOMARKER(S) DETECTED	THERAPY
Breast Cancer	<i>PIK3CA</i> mutations	ITOVEBI™ (inavolisib) in combination with palbociclib and fulvestrant
	<i>PIK3CA</i> mutations C420R, E542K, E545A, E545D [1635G>T only], E545G, E545K, Q546E, Q546R; and H1047L, H1047R, and H1047Y	PIQRAY® (alpelisib)
Colorectal Cancer (CRC)	<i>BRAF</i> V600E	BRAFTOVI® (encorafenib) in combination with cetuximab
Non-small cell lung cancer (NSCLC)	<i>ALK</i> rearrangements	ALECENSA® (alectinib)
	<i>BRAF</i> V600E	BRAFTOVI® (encorafenib) in combination with MEKTOVI® (binimetinib)
	<i>EGFR</i> Exon 19 deletions and <i>EGFR</i> Exon 21 L858R substitution	EGFR Tyrosine Kinase Inhibitors (TKI) Approved by FDA*
	<i>MET</i> single nucleotide variants (SNVs) and indels that lead to <i>MET</i> exon 14 skipping	TABRECTA® (capmatinib)
		TEPMETKO® (tepotinib)**
	<i>ROS1</i> fusions**	ROZLYTREK® (entrectinib)
Prostate cancer	<i>BRCA1</i> , <i>BRCA2</i> , <i>ATM</i> alterations	LYNPARZA® (olaparib)
	<i>BRCA1</i> , <i>BRCA2</i> alterations	AKEEGA® (niraparib + abiraterone acetate)
		LYNPARZA® (olaparib) in combination with abiraterone
		RUBRACA® (rucaparib)
	Homologous Recombination (HRR) gene (<i>BRCA1</i> , <i>BRCA2</i> , <i>ATM</i> , <i>ATR</i> , <i>CDK12</i> , <i>CHEK2</i> , <i>FANCA</i> , <i>MLH1</i> , <i>MRE11A</i> , <i>NBN</i> , <i>PALB2</i> , <i>RAD51C</i>) alterations	TALZENNA® (talazoparib) in combination with XTANDI® (enzalutamide)
Solid Tumors	<i>NTRK1/2/3</i> fusions**	ROZLYTREK® (entrectinib)

*For the most current information about the therapeutic products in this group, go to: https://www.fda.gov/medical-devices/in-vitro-diagnostics/list-cleared-or-approved-companion-diagnostic-devices-in-vitro-and-imaging-tools#Group_Labeling

**Note: When considering eligibility for ROZLYTREK® based on the detection of *NTRK1/2/3* and *ROS1* fusions, or for TEPMETKO® based on the detection of *MET* SNVs and indels that lead to *MET* exon 14 skipping, testing using plasma specimens is only appropriate for patients for whom tumor tissue is not available for testing.

ORDERED TEST #

APPENDIX

About FoundationOne® Liquid CDx

TEST PRINCIPLE

The FoundationOne Liquid CDx assay is performed exclusively at Foundation Medicine, Inc. owned and operated sites using circulating cfDNA isolated from plasma derived from anti-coagulated peripheral whole blood from patients with solid malignant neoplasms. The assay employs a single DNA extraction method to obtain cfDNA from plasma from whole blood. Extracted cfDNA undergoes whole-genome shotgun library construction and hybridization-based capture of 324 cancer-related genes. All coding exons of 309 genes are targeted; select intronic or non-coding regions are targeted in 15 of these genes (refer to Table 3 for the complete list of genes reported by FoundationOne Liquid CDx). Hybrid-capture selected libraries are sequenced with deep coverage using the NovaSeq® 6000 platform. Sequence data are processed using a custom analysis pipeline designed to detect genomic alterations, including base substitutions and indels in 311 genes, copy number variants in 3 genes, and genomic rearrangements in 8 genes. A subset of targeted regions in 75 genes is baited for enhanced sensitivity.

PERFORMANCE CHARACTERISTICS

Please refer to product label:
foundationmedicine.com/F1LCDx

WARNINGS AND PRECAUTIONS

1. Alterations reported may include somatic (not inherited) or germline (inherited) alterations; however, the test does not distinguish between germline and somatic alterations. If a reported alteration is suspected to be germline, confirmatory testing should be considered in the appropriate clinical context.
2. The test is not intended to replace germline testing or to provide information about cancer predisposition.
3. Patients for whom no companion diagnostic alterations are detected should be considered for confirmation with an FDA-approved tumor tissue test, if available.

LIMITATIONS

1. For *in vitro* diagnostic use.
2. For prescription use only. This test must be ordered by a qualified medical professional in accordance with clinical laboratory regulations.
3. Genomic findings other than those listed in Table 1 of the intended use are not prescriptive or conclusive for labeled use of any specific therapeutic product.
4. A negative result does not rule out the presence of an alteration in the patient's tumor.
5. Decisions on patient care and treatment must

be based on the independent medical judgment of the treating physician, taking into consideration all applicable information concerning the patient's condition, such as patient and family history, physical examinations, information from other diagnostic tests, and patient preferences, in accordance with the standard of care in a given community.

6. The test is intended to be performed on specific serial number-controlled instruments by Foundation Medicine, Inc.
7. Genomic findings from cfDNA may originate from circulating tumor DNA fragments, germline alterations, or nontumor somatic alterations, such as clonal hematopoiesis of indeterminate potential (CHIP). Genes with alterations that may be derived from CHIP include, but are not limited to, the following: *ASXL1*, *ATM*, *CBL*, *CHEK2*, *DNMT3A*, *JAK2*, *KMT2D* (*MLL2*), *MPL*, *MYD88*, *SF3B1*, *TET2*, *TP53*, and *U2AF1*. The efficacy of targeting such nontumor somatic alterations (e.g., CH) is unknown.
8. The analytical accuracy for the FoundationOne Liquid CDx assay has not been demonstrated in all genes.
9. The analytical accuracy for the FoundationOne Liquid CDx assay for the detection of SNVs and indels that lead to *MET* exon 14 skipping has not been demonstrated for samples with variant allele frequencies (VAF) below 0.34% for base substitutions and 0.73% VAF for small insertions and small deletions.
10. TABRECTA® efficacy has not been established in patients with *MET* SNVs <0.21% VAF and in patients with *MET* indels <0.16% VAF tested with FoundationOne Liquid CDx.
11. TEPMETKO® efficacy has not been established in patients with *MET* SNVs <0.19% VAF and in patients with *MET* indels <0.10% VAF tested with FoundationOne Liquid CDx.
12. ALECENSA® efficacy has not been established in patients with *ALK* rearrangements <0.06% VAF tested with FoundationOne Liquid CDx.
13. LYNPARZA® efficacy has not been established in prostate cancer patients with *BRCA1/2* or *ATM* rearrangements with <0.25% VAF or with short variants in *BRCA1/2* or *ATM* <0.11% VAF tested with FoundationOne Liquid CDx.
14. RUBRACA® efficacy has not been established in prostate cancer patients with *BRCA1/2* rearrangements with <0.85% VAF or with short variants in *BRCA1/2* <0.15% VAF tested with FoundationOne Liquid CDx.
15. PIQRAY® efficacy has not been established in patients with PIK3CA SNVs with <0.14% VAF

tested with FoundationOne Liquid CDx.

16. BRAF TOVI® (encorafenib) in combination with cetuximab efficacy has not been established in patients with the *BRAF* V600E alteration with <0.11% VAF tested with FoundationOne Liquid CDx.
17. BRAF TOVI® (encorafenib) in combination with MEK TOVI® (binimetinib) efficacy has not been established in patients with *BRAF* V600E with <0.099% VAF tested with FoundationOne Liquid CDx.
18. The precision of FoundationOne Liquid CDx was only confirmed for select variants at the limit of detection (LoD).
19. The FoundationOne Liquid CDx assay does not detect heterozygous deletions.
20. The FoundationOne Liquid CDx assay does not detect copy number losses/homozygous deletions in *ATM*, *ATR*, *CDK12*, *CHEK2*, *FANCA*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, and *RAD51C*. The prevalence of homozygous deletions in these genes ranges from 0–2.83% based on TALAPRO-2 trial data and 0–1.64% based on publicly available prostate cancer databases.
21. A complete assessment of the impact of cfDNA blood collection tube lot-to-lot variability on the performance of the test has not been evaluated.
22. The test is not intended to provide information on cancer predisposition.
23. *BRCA1/BRCA2* homozygous deletions and rearrangements were not adequately represented in all analytical studies.
24. Representation of *ALK* rearrangements were limited in the analytical validation studies.
25. The representation of short variants and rearrangements in *ATM*, *ATR*, *CDK12*, *CHEK2*, *FANCA*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, and *RAD51C* was limited in the analytical validation studies.
26. Performance has not been validated for cfDNA input below the specified minimum input.
27. Representation of SNV and indels that lead to *MET* exon 14 skipping that represent biomarker rule category 1 and 2, were limited in the analytical validation studies.
28. For optimal ctDNA shed, it is recommended that blood be drawn prior to therapy or at a time of disease progression. The sensitivity of liquid biopsy is related to adequate levels of ctDNA shed. Therefore, assay performance will be dependent upon level of ctDNA shed at time of testing.
29. Due to the low prevalence of *ROS1* fusions and *NTRK1/2/3* fusions, the positive predictive value (PPV) of the test (FoundationOne Liquid CDx positive, tissue negative) may be lower than reported in test labeling.

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ORDERED TEST

APPENDIX

About FoundationOne® Liquid CDx

30. FoundationOne Liquid CDx may miss a subset of patients with *NTRK1/2/3* fusion and *ROS1* fusion positive solid tumors who may derive benefit from ROZLYTREK®. In a retrospective-prospective clinical study assessing concordance between FoundationOne Liquid CDx test results in plasma and patients whose tumor tissue tested positive and was the basis for enrollment into a clinical trial, the data demonstrated that the FoundationOne Liquid CDx test did not detect approximately 46% of potential responders with *NTRK1/2/3* fusions and 49% of responders with *ROS1* fusions.
31. ROZLYTREK® efficacy has not been established in patients with *NTRK2* fusions tested with FoundationOne Liquid CDx, given the low prevalence of the biomarker.
32. In a retrospective-prospective clinical study assessing concordance between FoundationOne Liquid CDx test results in plasma and patients whose tumor tissue tested positive and was the basis for enrollment into a clinical trial, FoundationOne Liquid CDx detected 1 of 7 different *NTRK3* fusion partners. Due to the rarity of these fusions, the accuracy of FoundationOne Liquid CDx for *NTRK3* fusions has not been adequately determined.
33. *NTRK2* fusions per the FoundationOne Liquid CDx biomarker rules for *NTRK1/2/3* fusions were not represented in analytical validation studies.
34. A study evaluating the concordance to a second method demonstrated that the agreement between FoundationOne Liquid CDx positive results and a comparator method for *NTRK1/3*, and *ROS1* was $\leq 50\%$ (i.e., whether these are potential FoundationOne Liquid CDx false positives or false negatives by the comparator is unknown).
35. FoundationOne Liquid CDx may not detect a subset of patients with prostate cancer with *BRCA1/2* homozygous deletions who may derive benefit from AKEEGA. A subgroup analysis indicated that the FoundationOne Liquid CDx test did not detect approximately 81% (21/26) of prostate cancer patients with *BRCA1/2* homozygous deletions detected by FoundationOne CDx who derived benefit from AKEEGA. All samples were below the limit of detection for *BRCA2* copy number loss by the FoundationOne Liquid CDx assay. Additional testing to confirm the absence of *BRCA1/2* homozygous deletions in the patient's tumor tissue with another FDA approved test, if feasible, is strongly recommended. (Around 2.72% of patients with prostate cancer are expected to harbor *BRCA1/2* homozygous deletions, based on FMI internal data).
36. Results reported may include variants with

very low variant allele frequency (SNVs $<0.5\%$ VAF and indels $<1.0\%$ VAF). Such alterations may be false positive results detected due to background signals inherent in sequencing methods designed for high sensitivity or due to clonal hematopoiesis of indeterminate potential (CHIP). Additional clinical investigation to confirm the presence of these variants in the patient's tumor with another FDA-approved or cleared test is strongly recommended.

37. *BRCA1/2* homozygous deletions may not be detected in a subset of prostate cancer patients by FoundationOne Liquid CDx. Additional testing to confirm the absence of *BRCA1/2* homozygous deletions in the patient's tumor tissue with another FDA approved test, if feasible, is strongly recommended.
38. FoundationOne Liquid CDx may miss a subset of patients with *MET* single nucleotide variants (SNVs) and indels that lead to *MET* exon 14 skipping alterations in NSCLC patients who may derive benefit from TEPMETKO®. In a retrospective clinical study assessing concordance between FoundationOne Liquid CDx test results in plasma and patients whose plasma or tumor tissue tested positive and was the basis for enrollment into a clinical trial, the data demonstrated that the FoundationOne Liquid CDx test did not detect approximately 33% of responders with *MET* single nucleotide variants (SNVs) and indels that lead to *MET* exon 14 skipping alterations. Non-detection of *MET* exon 14 skipping alterations in these samples was attributed to low tumor fraction.

LEVEL 1: COMPANION DIAGNOSTICS (CDx)

Clinical evidence should be presented from a prospectively designed clinical trial. Results can also be presented from a retrospective clinical bridging study demonstrating that the clinical endpoints are preserved using plasma samples in trials where enrollment was based on tissue test results. For follow-on markers, a clinical concordance study demonstrating non-inferiority to the original FDA-approved cfDNA-based companion diagnostic device (refer to Li, Meijuan. Statistical Methods for Clinical Validation of Follow-On Companion Diagnostic Devices via an External Concordance Study. *Statistics in Biopharmaceutical Research*. 8: 35-363, 2016) is required. In addition to the clinical validation, analytical validation for each specific Level 1 CDx biomarker should be presented.

LEVEL 2: cfDNA BIOMARKERS WITH STRONG EVIDENCE OF CLINICAL SIGNIFICANCE IN cfDNA

For a Level 2 claim of cfDNA biomarkers with

strong evidence of clinical significance, clinical validation needs to be from evidence presented with FDA-approved liquid biopsy companion diagnostic biomarkers for the specific tumor type at the biomarker or variant level. Such claims should also be supported by analytical performance for each biomarker from at least LoD, precision/reproducibility, and LoD studies.

LEVEL 3A: BIOMARKERS WITH EVIDENCE OF CLINICAL SIGNIFICANCE IN TISSUE SUPPORTED BY STRONG ANALYTICAL VALIDATION USING cfDNA AND CONCORDANCE BETWEEN cfDNA AND TISSUE

Clinical evidence can be provided from tissue-based companion diagnostics. This should also be supported by analytical validation (LoD, precision, analytical accuracy, and concordance study to a tissue-based test) for the specific tumor type at the biomarker or variant level, using a representative approach for SNVs and indels. Evidence evaluating concordance between cfDNA- and tissue-samples for FDA-approved tissue markers should be demonstrated using an FDA-approved tissue test or a validated tissue test.

LEVEL 3B: BIOMARKERS WITH EVIDENCE OF CLINICAL SIGNIFICANCE IN TISSUE SUPPORTED BY ANALYTICAL VALIDATION USING cfDNA

Clinical evidence can be provided from tissue-based companion diagnostics, with analytical validity supported by a representative approach for SNVs and indels from key analytical studies (such as LoD, accuracy, and precision).

LEVEL 4: OTHER BIOMARKERS WITH POTENTIAL CLINICAL SIGNIFICANCE

Biomarkers not categorized into Levels 1, 2, or 3 can be included under Level 4 for informational purposes or to be used to direct patients toward clinical trials for which they may be eligible. Such claims can be supported by clinical rationale for inclusion in the panel. Such rationale could also include peer-reviewed publications for genes/variants in tissue, variant information from well-curated public databases, or *in vitro* pre-clinical models. Analytical validation should be supported by a representative approach for SNVs and indels from key analytical studies (such as LoD, accuracy, and precision).

ASSAY CONFIGURATION SPECIFIC TO THIS ISSUED REPORT

MR Suite Version (RG) 8.11.0

MR Reporting Config Version 81

Analysis Pipeline Version v3.43.0

Computational Biology Suite Version 7.0.1

ORDERED TEST #

APPENDIX

About FoundationOne®Liquid CDx

TABLE 2: EFFICACY OF THE FOLLOWING COMPANION DIAGNOSTIC THERAPIES HAS NOT BEEN ESTABLISHED IN PATIENTS WITH VAF BELOW THAT TESTED WITH FOUNDATIONONE LIQUID CDx

THERAPY	TUMOR TYPE	BIOMARKER	VAF %*
TABRECTA® (capmatinib)	Non-small cell lung cancer (NSCLC)	MET SNVs	0.21%
		MET indels	0.16%
TEPMETKO® (tepotinib)	Non-small cell lung cancer (NSCLC)	MET SNVs	0.19%
		MET indels	0.10%
ALECENSA® (alectinib)	Non-small cell lung cancer (NSCLC)	ALK rearrangements	0.06%
LYNPARZA® (olaparib)	Prostate cancer	BRCA1/2 or ATM rearrangements	0.25%
		BRCA1/2 or ATM SNVs	0.11%
RUBRACA® (rucaparib)	Prostate cancer	BRCA1/2 rearrangements	0.85%
		BRCA1/2 SNVs	0.15%
PIQRAY® (alpelisib)	Breast cancer	PIK3CA SNVs	0.14%
BRAFTOVI® (encorafenib) in combination with cetuximab	Colorectal cancer	BRAF V600E	0.11%
BRAFTOVI® (encorafenib) in combination with MEKTOVI® (binimetinib)	Non-small cell lung cancer (NSCLC)	BRAF V600E	0.099%

*Lowest VAF% tested during clinical validation

ORDERED TEST #

APPENDIX

Genes assayed in FoundationOne® Liquid CDx

Table 3: The FoundationOne Liquid CDx assay interrogates 324 genes, including 309 genes with complete exonic (coding) coverage and 15 genes with only select noncoding coverage (indicated with an *). Select regions in 75 genes (indicated in bold) are captured with increased sensitivity. Genes are captured for increased sensitivity with complete exonic (coding) coverage unless otherwise noted.

ABL1 Exons 4-9	<i>ACVR1B</i>	AKT1 Exon 3	<i>AKT2</i>	<i>AKT3</i>	ALK Exons 20-29, Introns 18, 19	<i>ALOX12B</i>	<i>AMER1</i> (FAM123B or WTX)	APC
AR	ARAF Exons 4, 5, 7, 11, 13, 15, 16	<i>ARFRP1</i>	<i>ARID1A</i>	<i>ASXL1</i>	ATM	ATR	<i>ATRX</i>	<i>AURKA</i>
<i>AURKB</i>	<i>AXIN1</i>	<i>AXL</i>	<i>BAP1</i>	<i>BARD1</i>	<i>BCL2</i>	<i>BCL2L1</i>	<i>BCL2L2</i>	<i>BCL6</i>
<i>BCOR</i>	<i>BCORL1</i>	<i>BCR*</i> Introns 8, 13, 14	BRAF Exons 11-18, Introns 7-10	BRCA1 Introns 2, 7, 8, 12, 16, 19, 20	BRCA2 Intron 2	<i>BRD4</i>	<i>BRIP1</i>	<i>BTG1</i>
<i>BTG2</i>	BTK Exons 2, 15	<i>CALR</i>	<i>CARD11</i>	<i>CASP8</i>	<i>CBFB</i>	<i>CBL</i>	CCND1	<i>CCND2</i>
<i>CCND3</i>	<i>CCNE1</i>	<i>CD22</i>	<i>CD70</i>	<i>CD74*</i> Introns 6-8	<i>CD79A</i>	<i>CD79B</i>	CD274 (PD-L1)	<i>CDC73</i>
CDH1	CDK12	CDK4	CDK6	<i>CDK8</i>	<i>CDKN1A</i>	<i>CDKN1B</i>	CDKN2A	<i>CDKN2B</i>
<i>CDKN2C</i>	<i>CEBPA</i>	<i>CHEK1</i>	CHEK2	<i>CIC</i>	<i>CREBBP</i>	CRKL	<i>CSF1R</i>	<i>CSF3R</i>
<i>CTCF</i>	<i>CTNNA1</i>	CTNNB1 Exon 3	<i>CUL3</i>	<i>CUL4A</i>	<i>CXCR4</i>	<i>CYP17A1</i>	<i>DAXX</i>	<i>DDR1</i>
DDR2 Exons 5, 17, 18	<i>DIS3</i>	<i>DNMT3A</i>	<i>DOT1L</i>	<i>EED</i>	EGFR Introns 7, 15, 24-27	<i>EMSY</i> (C11orf30)	<i>EP300</i>	<i>EPHA3</i>
<i>EPHB1</i>	<i>EPHB4</i>	ERBB2	ERBB3 Exons 3, 6, 7, 8, 10, 12, 20, 21, 23, 24, 25	<i>ERBB4</i>	<i>ERCC4</i>	<i>ERG</i>	ERRFI1	ESR1 Exons 4-8
<i>ETV4*</i> Intron 8	<i>ETV5*</i> Introns 6, 7	ETV6* Introns 5, 6	<i>EWSR1*</i> Introns 7-13	EZH2 Exons 4, 16, 17, 18	<i>EZR*</i> Introns 9-11	<i>FANCA</i>	<i>FANCC</i>	<i>FANCG</i>
<i>FANCL</i>	<i>FAS</i>	<i>FBXW7</i>	<i>FGF10</i>	<i>FGF12</i>	<i>FGF14</i>	<i>FGF19</i>	<i>FGF23</i>	<i>FGF3</i>
<i>FGF4</i>	<i>FGF6</i>	FGFR1 Introns 1, 5, Intron 17	FGFR2 Intron 1, Intron 17	FGFR3 Exons 7, 9 (alternative designation exon 10), 14, 18, Intron 17	<i>FGFR4</i>	<i>FH</i>	<i>FLCN</i>	<i>FLT1</i>
FLT3 Exons 14, 15, 20	FOXL2	<i>FUBP1</i>	<i>GABRA6</i>	<i>GATA3</i>	<i>GATA4</i>	<i>GATA6</i>	<i>GID4</i> (C17orf39)	GNAI1 Exons 4, 5
<i>GNAI3</i>	GNAQ Exons 4, 5	GNAS Exons 1, 8	<i>GRM3</i>	<i>GSK3B</i>	<i>H3-3A</i> (H3F3A)	<i>HDAC1</i>	<i>HGF</i>	<i>HNF1A</i>
HRAS Exons 2, 3	<i>HSD3B1</i>	<i>ID3</i>	IDH1 Exon 4	IDH2 Exon 4	<i>IGF1R</i>	<i>IKBKE</i>	<i>IKZF1</i>	<i>INPP4B</i>
<i>IRF2</i>	<i>IRF4</i>	<i>IRS2</i>	<i>JAK1</i>	JAK2 Exon 14	JAK3 Exons 5, 11, 12, 13, 15, 16	<i>JUN</i>	<i>KDM5A</i>	<i>KDM5C</i>
<i>KDM6A</i>	<i>KDR</i>	<i>KEAP1</i>	<i>KEL</i>	KIT Exons 8, 9, 11, 12, 13, 17, Intron 16	<i>KLHL6</i>	<i>KMT2A</i> (MLL) Introns 6, 8-11, Intron 7	<i>KMT2D</i> (MLL2)	KRAS

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APPENDIX

Genes assayed in FoundationOne® Liquid CDx

Table 3: The FoundationOne Liquid CDx assay interrogates 324 genes, including 309 genes with complete exonic (coding) coverage and 15 genes with only select noncoding coverage (indicated with an *). Select regions in 75 genes (indicated in bold) are captured with increased sensitivity. Genes are captured for increased sensitivity with complete exonic (coding) coverage unless otherwise noted.

LTK	LYN	MAF	MAP2K1 (MEK1) Exons 2, 3	MAP2K2 (MEK2) Exons 2-4, 6, 7	MAP2K4	MAP3K1	MAP3K13	MAPK1
MCL1	MDM2	MDM4	MED12	MEF2B	MEN1	MERTK	MET	MITF
MKNK1	MLH1	MPL Exon 10	MRE11 (MRE11A)	MSH2 Intron 5	MSH3	MSH6	MST1R	MTAP
MTOR Exons 19, 30, 39, 40, 43-45, 47, 48, 53, 56	MUTYH	MYB* Intron 14	MYC Intron 1	MYCL (MYCL1)	MYCN	MYD88 Exon 4	NBN	NF1
NF2	NFE2L2	NFKBIA	NKX2-1	NOTCH1	NOTCH2 Intron 26	NOTCH3	NPM1 Exons 4-6, 8, 10	NRAS Exons 2, 3
NSD2 (WHSC1 or MMSET)	NSD3 (WHSC1L1)	NT5C2	NTRK1 Exons 14, 15, Introns 8-11	NTRK2 Intron 12	NTRK3 Exons 16, 17	NUTM1* Intron 1	P2RY8	PALB2
PARP1	PARP2	PARP3	PAX5	PBRM1	PDCD1 (PD-1)	PDCD1LG2 (PD-L2)	PDGFRA Exons 12, 18, Introns 7, 9, 11	PDGFRB Exons 12-21, 23
PDK1	PIK3C2B	PIK3C2G	PIK3CA Exons 2, 3, 5-8, 10, 14, 19, 21 (Coding Exons 1, 2, 4-7, 9, 13, 18, 20)	PIK3CB	PIK3R1	PIM1	PMS2	POLD1
POLE	PPARG	PPP2R1A	PPP2R2A	PRDM1	PRKAR1A	PRKCI	PRKN (PARK2)	PTCH1
PTEN	PTPN11	PTPRO	QKI	RAC1	RAD21	RAD51	RAD51B	RAD51C
RAD51D	RAD52	RAD54L	RAF1 Exons 3, 4, 6, 7, 10, 14, 15, 17, Introns 4-8	RARA Intron 2	RB1	RBM10	REL	RET Introns 7, 8, Exons 11, 13-16, Introns 9-11
RICTOR	RNF43	ROS1 Exons 31, 36-38, 40, Introns 31-35	RPTOR	RSPO2* Intron 1	SDC4* Intron 2	SDHA	SDHB	SDHC
SDHD	SETD2	SF3B1	SGK1	SLC34A2* Intron 4	SMAD2	SMAD4	SMARCA4	SMARCB1
SMO	SNCAIP	SOC1	SOX2	SOX9	SPEN	SPOP	SRC	STAG2
STAT3	STK11	SUFU	SYK	TBX3	TEK	TENT5C (FAM46C)	TERC* ncRNA	TERT* Promoter
TET2	TGFBR2	TIPARP	TMPRSS2* Introns 1-3	TNFAIP3	TNFRSF14	TP53	TSC1	TSC2
TYRO3	U2AF1	VEGFA	VHL	WTI	XPO1	XRCC2	ZNF217	ZNF703

PATIENT

DISEASE **Prostate cancer (NOS)**
NAME
DATE OF BIRTH
SEX
MEDICAL RECORD #

PHYSICIAN

ORDERING PHYSICIAN
MEDICAL FACILITY
ADDITIONAL RECIPIENT
MEDICAL FACILITY ID
PATHOLOGIST

SPECIMEN

SPECIMEN ID
SPECIMEN TYPE
DATE OF COLLECTION
SPECIMEN RECEIVED

FDA-Approved Content

Companion Diagnostic (CDx) Findings

A companion diagnostic provides essential information for the safe and effective use of a corresponding drug or biological product. This table contains therapies associated with FoundationOne®Liquid CDx's FDA-approved companion diagnostic indications.

GENOMIC FINDINGS
CDx-INDICATED THERAPIES

No Companion Diagnostic (CDx) alterations for FoundationOne®Liquid CDx were detected. Please consider confirmation with tumor tissue testing, such as FoundationOne®CDx, if possible.

Tumor Profiling Results

FoundationOne®Liquid CDx is FDA-approved to provide tumor mutation profiling results for oncology patients with solid tumors.

SHORT VARIANTS AND SELECT REARRANGEMENTS AND COPY NUMBER ALTERATIONS IDENTIFIED

Results reported in this section that are not designated as CDx findings are not prescriptive or conclusive for labeled use of any specific therapeutic product. See *professional services* section for information on the alterations listed in this section as well as any additional detected copy number alterations, gene rearrangements, or biomarkers. Please refer to the appendix for the description of the biomarker levels.

Other biomarkers with potential clinical significance

ATM L2452P #

Variants in this gene may be derived from a nontumor source such as clonal hematopoiesis (CH). The efficacy of targeting such nontumor somatic alterations (e.g., CH) is unknown.

Please refer to appendix for Explanation of Clinical Significance Classification and for variants of unknown significance (VUS).

ORDERED TEST #

APPENDIX

About FoundationOne®Liquid CDx

INTENDED USE

FoundationOne Liquid CDx is a qualitative next generation sequencing based *in vitro* diagnostic test that uses targeted high throughput hybridization-based capture technology to analyze 324 genes and report genomic alterations in 311 genes. These include substitutions, insertions and deletions (indels) in 311 genes, rearrangements in 8 genes and copy number alterations in 3 genes. FoundationOne Liquid CDx utilizes circulating cell-free DNA (cfDNA) isolated from plasma derived from anti-coagulated peripheral whole blood of cancer patients collected in FoundationOne Liquid CDx cfDNA blood collection tubes included in the FoundationOne Liquid CDx Blood Sample Collection Kit. The test is intended to be used as a companion diagnostic to identify patients who may benefit from treatment with the targeted therapies listed in Table 1 in accordance with the approved therapeutic product labeling.

Additionally, FoundationOne Liquid CDx is intended to provide tumor mutation profiling to be used by qualified health care professionals in accordance with professional guidelines in oncology for patients with solid malignant neoplasms.

A negative result from a plasma specimen does not mean that the patient's tumor is negative for genomic findings. Patients with the tumor types above who are negative for the mutations listed in Table 1 (see ** footnote under Table 1 for *NTRK1/2/3* and *ROS1* fusions for ROZLYTREK® and *MET* SNVs and indels that lead to *MET* exon 14 skipping for TEPMETKO®) should be reflexed to routine biopsy and their tumor mutation status confirmed using an FDA-approved tumor tissue test, if feasible.

Genomic findings other than those listed in Table 1 are not prescriptive or conclusive for labeled use of any specific therapeutic product.

TABLE 1: COMPANION DIAGNOSTIC INDICATIONS

TUMOR TYPE	BIOMARKER(S) DETECTED	THERAPY
Breast Cancer	<i>PIK3CA</i> mutations	ITOVEBI™ (inavolisib) in combination with palbociclib and fulvestrant
	<i>PIK3CA</i> mutations C420R, E542K, E545A, E545D [1635G>T only], E545G, E545K, Q546E, Q546R; and H1047L, H1047R, and H1047Y	PIQRAY® (alpelisib)
Colorectal Cancer (CRC)	<i>BRAF</i> V600E	BRAFTOVI® (encorafenib) in combination with cetuximab
Non-small cell lung cancer (NSCLC)	<i>ALK</i> rearrangements	ALECENSA® (alectinib)
	<i>BRAF</i> V600E	BRAFTOVI® (encorafenib) in combination with MEKTOVI® (binimetinib)
	<i>EGFR</i> Exon 19 deletions and <i>EGFR</i> Exon 21 L858R substitution	EGFR Tyrosine Kinase Inhibitors (TKI) Approved by FDA*
	<i>MET</i> single nucleotide variants (SNVs) and indels that lead to <i>MET</i> exon 14 skipping	TABRECTA® (capmatinib)
		TEPMETKO® (tepotinib)**
	<i>ROS1</i> fusions**	ROZLYTREK® (entrectinib)
Prostate cancer	<i>BRCA1</i> , <i>BRCA2</i> , <i>ATM</i> alterations	LYNPARZA® (olaparib)
	<i>BRCA1</i> , <i>BRCA2</i> alterations	AKEEGA® (niraparib + abiraterone acetate)
		LYNPARZA® (olaparib) in combination with abiraterone
		RUBRACA® (rucaparib)
	Homologous Recombination (HRR) gene (<i>BRCA1</i> , <i>BRCA2</i> , <i>ATM</i> , <i>ATR</i> , <i>CDK12</i> , <i>CHEK2</i> , <i>FANCA</i> , <i>MLH1</i> , <i>MRE11A</i> , <i>NBN</i> , <i>PALB2</i> , <i>RAD51C</i>) alterations	TALZENNA® (talazoparib) in combination with XTANDI® (enzalutamide)
Solid Tumors	<i>NTRK1/2/3</i> fusions**	ROZLYTREK® (entrectinib)

*For the most current information about the therapeutic products in this group, go to: https://www.fda.gov/medical-devices/in-vitro-diagnostics/list-cleared-or-approved-companion-diagnostic-devices-in-vitro-and-imaging-tools#Group_Labeling

**Note: When considering eligibility for ROZLYTREK® based on the detection of *NTRK1/2/3* and *ROS1* fusions, or for TEPMETKO® based on the detection of *MET* SNVs and indels that lead to *MET* exon 14 skipping, testing using plasma specimens is only appropriate for patients for whom tumor tissue is not available for testing.

ORDERED TEST #

APPENDIX
About FoundationOne® Liquid CDx
TEST PRINCIPLE

The FoundationOne Liquid CDx assay is performed exclusively at Foundation Medicine, Inc. owned and operated sites using circulating cfDNA isolated from plasma derived from anti-coagulated peripheral whole blood from patients with solid malignant neoplasms. The assay employs a single DNA extraction method to obtain cfDNA from plasma from whole blood. Extracted cfDNA undergoes whole-genome shotgun library construction and hybridization-based capture of 324 cancer-related genes. All coding exons of 309 genes are targeted; select intronic or non-coding regions are targeted in 15 of these genes (refer to Table 3 for the complete list of genes reported by FoundationOne Liquid CDx). Hybrid-capture selected libraries are sequenced with deep coverage using the NovaSeq® 6000 platform. Sequence data are processed using a custom analysis pipeline designed to detect genomic alterations, including base substitutions and indels in 311 genes, copy number variants in 3 genes, and genomic rearrangements in 8 genes. A subset of targeted regions in 75 genes is baited for enhanced sensitivity.

PERFORMANCE CHARACTERISTICS

Please refer to product label:
foundationmedicine.com/F1LCDx

WARNINGS AND PRECAUTIONS

1. Alterations reported may include somatic (not inherited) or germline (inherited) alterations; however, the test does not distinguish between germline and somatic alterations. If a reported alteration is suspected to be germline, confirmatory testing should be considered in the appropriate clinical context.
2. The test is not intended to replace germline testing or to provide information about cancer predisposition.
3. Patients for whom no companion diagnostic alterations are detected should be considered for confirmation with an FDA-approved tumor tissue test, if available.

LIMITATIONS

1. For *in vitro* diagnostic use.
2. For prescription use only. This test must be ordered by a qualified medical professional in accordance with clinical laboratory regulations.
3. Genomic findings other than those listed in Table 1 of the intended use are not prescriptive or conclusive for labeled use of any specific therapeutic product.
4. A negative result does not rule out the presence of an alteration in the patient's tumor.
5. Decisions on patient care and treatment must

be based on the independent medical judgment of the treating physician, taking into consideration all applicable information concerning the patient's condition, such as patient and family history, physical examinations, information from other diagnostic tests, and patient preferences, in accordance with the standard of care in a given community.

6. The test is intended to be performed on specific serial number-controlled instruments by Foundation Medicine, Inc.
7. Genomic findings from cfDNA may originate from circulating tumor DNA fragments, germline alterations, or nontumor somatic alterations, such as clonal hematopoiesis of indeterminate potential (CHIP). Genes with alterations that may be derived from CHIP include, but are not limited to, the following: *ASXL1*, *ATM*, *CBL*, *CHEK2*, *DNMT3A*, *JAK2*, *KMT2D* (*MLL2*), *MPL*, *MYD88*, *SF3B1*, *TET2*, *TP53*, and *U2AF1*. The efficacy of targeting such nontumor somatic alterations (e.g., CH) is unknown.
8. The analytical accuracy for the FoundationOne Liquid CDx assay has not been demonstrated in all genes.
9. The analytical accuracy for the FoundationOne Liquid CDx assay for the detection of SNVs and indels that lead to *MET* exon 14 skipping has not been demonstrated for samples with variant allele frequencies (VAF) below 0.34% for base substitutions and 0.73% VAF for small insertions and small deletions.
10. TABRECTA® efficacy has not been established in patients with *MET* SNVs <0.21% VAF and in patients with *MET* indels <0.16% VAF tested with FoundationOne Liquid CDx.
11. TEPMETKO® efficacy has not been established in patients with *MET* SNVs <0.19% VAF and in patients with *MET* indels <0.10% VAF tested with FoundationOne Liquid CDx.
12. ALECENSA® efficacy has not been established in patients with *ALK* rearrangements <0.06% VAF tested with FoundationOne Liquid CDx.
13. LYNPARZA® efficacy has not been established in prostate cancer patients with *BRCA1/2* or *ATM* rearrangements with <0.25% VAF or with short variants in *BRCA1/2* or *ATM* <0.11% VAF tested with FoundationOne Liquid CDx.
14. RUBRACA® efficacy has not been established in prostate cancer patients with *BRCA1/2* rearrangements with <0.85% VAF or with short variants in *BRCA1/2* <0.15% VAF tested with FoundationOne Liquid CDx.
15. PIQRAY® efficacy has not been established in patients with PIK3CA SNVs with <0.14% VAF

tested with FoundationOne Liquid CDx.

16. BRAF TOVI® (encorafenib) in combination with cetuximab efficacy has not been established in patients with the *BRAF* V600E alteration with <0.11% VAF tested with FoundationOne Liquid CDx.
17. BRAF TOVI® (encorafenib) in combination with MEK TOVI® (binimetinib) efficacy has not been established in patients with *BRAF* V600E with <0.099% VAF tested with FoundationOne Liquid CDx.
18. The precision of FoundationOne Liquid CDx was only confirmed for select variants at the limit of detection (LoD).
19. The FoundationOne Liquid CDx assay does not detect heterozygous deletions.
20. The FoundationOne Liquid CDx assay does not detect copy number losses/homozygous deletions in *ATM*, *ATR*, *CDK12*, *CHEK2*, *FANCA*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, and *RAD51C*. The prevalence of homozygous deletions in these genes ranges from 0–2.83% based on TALAPRO-2 trial data and 0–1.64% based on publicly available prostate cancer databases.
21. A complete assessment of the impact of cfDNA blood collection tube lot-to-lot variability on the performance of the test has not been evaluated.
22. The test is not intended to provide information on cancer predisposition.
23. *BRCA1/BRCA2* homozygous deletions and rearrangements were not adequately represented in all analytical studies.
24. Representation of *ALK* rearrangements were limited in the analytical validation studies.
25. The representation of short variants and rearrangements in *ATM*, *ATR*, *CDK12*, *CHEK2*, *FANCA*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, and *RAD51C* was limited in the analytical validation studies.
26. Performance has not been validated for cfDNA input below the specified minimum input.
27. Representation of SNV and indels that lead to *MET* exon 14 skipping that represent biomarker rule category 1 and 2, were limited in the analytical validation studies.
28. For optimal ctDNA shed, it is recommended that blood be drawn prior to therapy or at a time of disease progression. The sensitivity of liquid biopsy is related to adequate levels of ctDNA shed. Therefore, assay performance will be dependent upon level of ctDNA shed at time of testing.
29. Due to the low prevalence of *ROS1* fusions and *NTRK1/2/3* fusions, the positive predictive value (PPV) of the test (FoundationOne Liquid CDx positive, tissue negative) may be lower than reported in test labeling.

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Sample Analysis: 150 Second St., 1st Floor, Cambridge, MA 02141 • CLIA: 22D2027531
Post-Sequencing Analysis: 150 Second St., 1st Floor, Cambridge, MA 02141 • CLIA: 22D2027531

ORDERED TEST

APPENDIX

About FoundationOne®Liquid CDx

30. FoundationOne Liquid CDx may miss a subset of patients with *NTRK1/2/3* fusion and *ROS1* fusion positive solid tumors who may derive benefit from ROZLYTREK®. In a retrospective-prospective clinical study assessing concordance between FoundationOne Liquid CDx test results in plasma and patients whose tumor tissue tested positive and was the basis for enrollment into a clinical trial, the data demonstrated that the FoundationOne Liquid CDx test did not detect approximately 46% of potential responders with *NTRK1/2/3* fusions and 49% of responders with *ROS1* fusions.
31. ROZLYTREK® efficacy has not been established in patients with *NTRK2* fusions tested with FoundationOne Liquid CDx, given the low prevalence of the biomarker.
32. In a retrospective-prospective clinical study assessing concordance between FoundationOne Liquid CDx test results in plasma and patients whose tumor tissue tested positive and was the basis for enrollment into a clinical trial, FoundationOne Liquid CDx detected 1 of 7 different *NTRK3* fusion partners. Due to the rarity of these fusions, the accuracy of FoundationOne Liquid CDx for *NTRK3* fusions has not been adequately determined.
33. *NTRK2* fusions per the FoundationOne Liquid CDx biomarker rules for *NTRK1/2/3* fusions were not represented in analytical validation studies.
34. A study evaluating the concordance to a second method demonstrated that the agreement between FoundationOne Liquid CDx positive results and a comparator method for *NTRK1/3*, and *ROS1* was $\leq 50\%$ (i.e., whether these are potential FoundationOne Liquid CDx false positives or false negatives by the comparator is unknown).
35. FoundationOne Liquid CDx may not detect a subset of patients with prostate cancer with *BRCA1/2* homozygous deletions who may derive benefit from AKEEGA. A subgroup analysis indicated that the FoundationOne Liquid CDx test did not detect approximately 81% (21/26) of prostate cancer patients with *BRCA1/2* homozygous deletions detected by FoundationOne CDx who derived benefit from AKEEGA. All samples were below the limit of detection for *BRCA2* copy number loss by the FoundationOne Liquid CDx assay. Additional testing to confirm the absence of *BRCA1/2* homozygous deletions in the patient's tumor tissue with another FDA approved test, if feasible, is strongly recommended. (Around 2.72% of patients with prostate cancer are expected to harbor *BRCA1/2* homozygous deletions, based on FMI internal data).
36. Results reported may include variants with

very low variant allele frequency (SNVs $<0.5\%$ VAF and indels $<1.0\%$ VAF). Such alterations may be false positive results detected due to background signals inherent in sequencing methods designed for high sensitivity or due to clonal hematopoiesis of indeterminate potential (CHIP). Additional clinical investigation to confirm the presence of these variants in the patient's tumor with another FDA-approved or cleared test is strongly recommended.

37. *BRCA1/2* homozygous deletions may not be detected in a subset of prostate cancer patients by FoundationOne Liquid CDx. Additional testing to confirm the absence of *BRCA1/2* homozygous deletions in the patient's tumor tissue with another FDA approved test, if feasible, is strongly recommended.
38. FoundationOne Liquid CDx may miss a subset of patients with *MET* single nucleotide variants (SNVs) and indels that lead to *MET* exon 14 skipping alterations in NSCLC patients who may derive benefit from TEPMETKO®. In a retrospective clinical study assessing concordance between FoundationOne Liquid CDx test results in plasma and patients whose plasma or tumor tissue tested positive and was the basis for enrollment into a clinical trial, the data demonstrated that the FoundationOne Liquid CDx test did not detect approximately 33% of responders with *MET* single nucleotide variants (SNVs) and indels that lead to *MET* exon 14 skipping alterations. Non-detection of *MET* exon 14 skipping alterations in these samples was attributed to low tumor fraction.

LEVEL 1: COMPANION DIAGNOSTICS (CDx)

Clinical evidence should be presented from a prospectively designed clinical trial. Results can also be presented from a retrospective clinical bridging study demonstrating that the clinical endpoints are preserved using plasma samples in trials where enrollment was based on tissue test results. For follow-on markers, a clinical concordance study demonstrating non-inferiority to the original FDA-approved cfDNA-based companion diagnostic device (refer to Li, Meijuan. Statistical Methods for Clinical Validation of Follow-On Companion Diagnostic Devices via an External Concordance Study. *Statistics in Biopharmaceutical Research*. 8: 35-363, 2016) is required. In addition to the clinical validation, analytical validation for each specific Level 1 CDx biomarker should be presented.

LEVEL 2: cfDNA BIOMARKERS WITH STRONG EVIDENCE OF CLINICAL SIGNIFICANCE IN cfDNA

For a Level 2 claim of cfDNA biomarkers with

strong evidence of clinical significance, clinical validation needs to be from evidence presented with FDA-approved liquid biopsy companion diagnostic biomarkers for the specific tumor type at the biomarker or variant level. Such claims should also be supported by analytical performance for each biomarker from at least LoD, precision/reproducibility, and LoD studies.

LEVEL 3A: BIOMARKERS WITH EVIDENCE OF CLINICAL SIGNIFICANCE IN TISSUE SUPPORTED BY STRONG ANALYTICAL VALIDATION USING cfDNA AND CONCORDANCE BETWEEN cfDNA AND TISSUE

Clinical evidence can be provided from tissue-based companion diagnostics. This should also be supported by analytical validation (LoD, precision, analytical accuracy, and concordance study to a tissue-based test) for the specific tumor type at the biomarker or variant level, using a representative approach for SNVs and indels. Evidence evaluating concordance between cfDNA- and tissue-samples for FDA-approved tissue markers should be demonstrated using an FDA-approved tissue test or a validated tissue test.

LEVEL 3B: BIOMARKERS WITH EVIDENCE OF CLINICAL SIGNIFICANCE IN TISSUE SUPPORTED BY ANALYTICAL VALIDATION USING cfDNA

Clinical evidence can be provided from tissue-based companion diagnostics, with analytical validity supported by a representative approach for SNVs and indels from key analytical studies (such as LoD, accuracy, and precision).

LEVEL 4: OTHER BIOMARKERS WITH POTENTIAL CLINICAL SIGNIFICANCE

Biomarkers not categorized into Levels 1, 2, or 3 can be included under Level 4 for informational purposes or to be used to direct patients toward clinical trials for which they may be eligible. Such claims can be supported by clinical rationale for inclusion in the panel. Such rationale could also include peer-reviewed publications for genes/variants in tissue, variant information from well-curated public databases, or *in vitro* pre-clinical models. Analytical validation should be supported by a representative approach for SNVs and indels from key analytical studies (such as LoD, accuracy, and precision).

ASSAY CONFIGURATION SPECIFIC TO THIS ISSUED REPORT

MR Suite Version (RG) 8.11.0

MR Reporting Config Version 81

Analysis Pipeline Version v3.43.0

Computational Biology Suite Version 7.0.1

ORDERED TEST #

APPENDIX

About FoundationOne®Liquid CDx

TABLE 2: EFFICACY OF THE FOLLOWING COMPANION DIAGNOSTIC THERAPIES HAS NOT BEEN ESTABLISHED IN PATIENTS WITH VAF BELOW THAT TESTED WITH FOUNDATIONONE LIQUID CDx

THERAPY	TUMOR TYPE	BIOMARKER	VAF %*
TABRECTA® (capmatinib)	Non-small cell lung cancer (NSCLC)	MET SNVs	0.21%
		MET indels	0.16%
TEPMETKO® (tepotinib)	Non-small cell lung cancer (NSCLC)	MET SNVs	0.19%
		MET indels	0.10%
ALECENSA® (alectinib)	Non-small cell lung cancer (NSCLC)	ALK rearrangements	0.06%
LYNPARZA® (olaparib)	Prostate cancer	BRCA1/2 or ATM rearrangements	0.25%
		BRCA1/2 or ATM SNVs	0.11%
RUBRACA® (rucaparib)	Prostate cancer	BRCA1/2 rearrangements	0.85%
		BRCA1/2 SNVs	0.15%
PIQRAY® (alpelisib)	Breast cancer	PIK3CA SNVs	0.14%
BRAFTOVI® (encorafenib) in combination with cetuximab	Colorectal cancer	BRAF V600E	0.11%
BRAFTOVI® (encorafenib) in combination with MEKTOVI® (binimetinib)	Non-small cell lung cancer (NSCLC)	BRAF V600E	0.099%

*Lowest VAF% tested during clinical validation

ORDERED TEST #

APPENDIX

Genes assayed in FoundationOne® Liquid CDx

Table 3: The FoundationOne Liquid CDx assay interrogates 324 genes, including 309 genes with complete exonic (coding) coverage and 15 genes with only select noncoding coverage (indicated with an *). Select regions in 75 genes (indicated in bold) are captured with increased sensitivity. Genes are captured for increased sensitivity with complete exonic (coding) coverage unless otherwise noted.

ABL1 Exons 4-9	<i>ACVR1B</i>	AKT1 Exon 3	<i>AKT2</i>	<i>AKT3</i>	ALK Exons 20-29, Introns 18, 19	<i>ALOX12B</i>	<i>AMER1</i> (FAM123B or WTX)	APC
AR	ARAF Exons 4, 5, 7, 11, 13, 15, 16	<i>ARFRP1</i>	<i>ARID1A</i>	<i>ASXL1</i>	ATM	ATR	<i>ATRX</i>	<i>AURKA</i>
<i>AURKB</i>	<i>AXIN1</i>	<i>AXL</i>	<i>BAP1</i>	<i>BARD1</i>	<i>BCL2</i>	<i>BCL2L1</i>	<i>BCL2L2</i>	<i>BCL6</i>
<i>BCOR</i>	<i>BCORL1</i>	<i>BCR*</i> Introns 8, 13, 14	BRAF Exons 11-18, Introns 7-10	BRCA1 Introns 2, 7, 8, 12, 16, 19, 20	BRCA2 Intron 2	<i>BRD4</i>	<i>BRIP1</i>	<i>BTG1</i>
<i>BTG2</i>	BTK Exons 2, 15	<i>CALR</i>	<i>CARD11</i>	<i>CASP8</i>	<i>CBFB</i>	<i>CBL</i>	CCND1	<i>CCND2</i>
<i>CCND3</i>	<i>CCNE1</i>	<i>CD22</i>	<i>CD70</i>	<i>CD74*</i> Introns 6-8	<i>CD79A</i>	<i>CD79B</i>	CD274 (PD-L1)	<i>CDC73</i>
CDH1	CDK12	CDK4	CDK6	<i>CDK8</i>	<i>CDKN1A</i>	<i>CDKN1B</i>	CDKN2A	<i>CDKN2B</i>
<i>CDKN2C</i>	<i>CEBPA</i>	<i>CHEK1</i>	CHEK2	<i>CIC</i>	<i>CREBBP</i>	CRKL	<i>CSF1R</i>	<i>CSF3R</i>
<i>CTCF</i>	<i>CTNNA1</i>	CTNNB1 Exon 3	<i>CUL3</i>	<i>CUL4A</i>	<i>CXCR4</i>	<i>CYP17A1</i>	<i>DAXX</i>	<i>DDR1</i>
DDR2 Exons 5, 17, 18	<i>DIS3</i>	<i>DNMT3A</i>	<i>DOT1L</i>	<i>EED</i>	EGFR Introns 7, 15, 24-27	<i>EMSY</i> (C11orf30)	<i>EP300</i>	<i>EPHA3</i>
<i>EPHB1</i>	<i>EPHB4</i>	ERBB2	ERBB3 Exons 3, 6, 7, 8, 10, 12, 20, 21, 23, 24, 25	<i>ERBB4</i>	<i>ERCC4</i>	<i>ERG</i>	ERRFI1	ESR1 Exons 4-8
<i>ETV4*</i> Intron 8	<i>ETV5*</i> Introns 6, 7	ETV6* Introns 5, 6	<i>EWSR1*</i> Introns 7-13	EZH2 Exons 4, 16, 17, 18	<i>EZR*</i> Introns 9-11	<i>FANCA</i>	<i>FANCC</i>	<i>FANCG</i>
<i>FANCL</i>	<i>FAS</i>	<i>FBXW7</i>	<i>FGF10</i>	<i>FGF12</i>	<i>FGF14</i>	<i>FGF19</i>	<i>FGF23</i>	<i>FGF3</i>
<i>FGF4</i>	<i>FGF6</i>	FGFR1 Introns 1, 5, Intron 17	FGFR2 Intron 1, Intron 17	FGFR3 Exons 7, 9 (alternative designation exon 10), 14, 18, Intron 17	<i>FGFR4</i>	<i>FH</i>	<i>FLCN</i>	<i>FLT1</i>
FLT3 Exons 14, 15, 20	FOXL2	<i>FUBP1</i>	<i>GABRA6</i>	<i>GATA3</i>	<i>GATA4</i>	<i>GATA6</i>	<i>GID4</i> (C17orf39)	GNAI1 Exons 4, 5
<i>GNAI3</i>	GNAQ Exons 4, 5	GNAS Exons 1, 8	<i>GRM3</i>	<i>GSK3B</i>	<i>H3-3A</i> (H3F3A)	<i>HDAC1</i>	<i>HGF</i>	<i>HNF1A</i>
HRAS Exons 2, 3	<i>HSD3B1</i>	<i>ID3</i>	IDH1 Exon 4	IDH2 Exon 4	<i>IGF1R</i>	<i>IKBKE</i>	<i>IKZF1</i>	<i>INPP4B</i>
<i>IRF2</i>	<i>IRF4</i>	<i>IRS2</i>	<i>JAK1</i>	JAK2 Exon 14	JAK3 Exons 5, 11, 12, 13, 15, 16	<i>JUN</i>	<i>KDM5A</i>	<i>KDM5C</i>
<i>KDM6A</i>	<i>KDR</i>	<i>KEAP1</i>	<i>KEL</i>	KIT Exons 8, 9, 11, 12, 13, 17, Intron 16	<i>KLHL6</i>	<i>KMT2A</i> (MLL) Introns 6, 8-11, Intron 7	<i>KMT2D</i> (MLL2)	KRAS

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Electronically signed by Caleb Ho, M.D. |
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ORDERED TEST #

APPENDIX

Genes assayed in FoundationOne® Liquid CDx

Table 3: The FoundationOne Liquid CDx assay interrogates 324 genes, including 309 genes with complete exonic (coding) coverage and 15 genes with only select noncoding coverage (indicated with an *). Select regions in 75 genes (indicated in bold) are captured with increased sensitivity. Genes are captured for increased sensitivity with complete exonic (coding) coverage unless otherwise noted.

<i>LTK</i>	<i>LYN</i>	<i>MAF</i>	MAP2K1 (MEK1) Exons 2, 3	MAP2K2 (MEK2) Exons 2-4, 6, 7	<i>MAP2K4</i>	<i>MAP3K1</i>	<i>MAP3K13</i>	<i>MAPK1</i>
<i>MCL1</i>	MDM2	<i>MDM4</i>	<i>MED12</i>	<i>MEF2B</i>	<i>MEN1</i>	<i>MERTK</i>	MET	<i>MITF</i>
<i>MKNK1</i>	<i>MLH1</i>	MPL Exon 10	<i>MRE11</i> (MRE11A)	<i>MSH2</i> Intron 5	<i>MSH3</i>	<i>MSH6</i>	<i>MST1R</i>	<i>MTAP</i>
MTOR Exons 19, 30, 39, 40, 43-45, 47, 48, 53, 56	<i>MUTYH</i>	<i>MYB*</i> Intron 14	MYC Intron 1	<i>MYCL</i> (MYCL1)	MYCN	MYD88 Exon 4	<i>NBN</i>	NF1
<i>NF2</i>	<i>NFE2L2</i>	<i>NFKBIA</i>	<i>NKX2-1</i>	<i>NOTCH1</i>	<i>NOTCH2</i> Intron 26	<i>NOTCH3</i>	NPM1 Exons 4-6, 8, 10	NRAS Exons 2, 3
<i>NSD2</i> (WHSC1 or MMSET)	<i>NSD3</i> (WHSC1L1)	<i>NT5C2</i>	NTRK1 Exons 14, 15, Introns 8-11	<i>NTRK2</i> Intron 12	NTRK3 Exons 16, 17	<i>NUTM1*</i> Intron 1	<i>P2RY8</i>	PALB2
<i>PARP1</i>	<i>PARP2</i>	<i>PARP3</i>	<i>PAX5</i>	<i>PBRM1</i>	<i>PDCD1</i> (PD-1)	PDCD1LG2 (PD-L2)	PDGFRA Exons 12, 18, Introns 7, 9, 11	PDGFRB Exons 12-21, 23
<i>PDK1</i>	<i>PIK3C2B</i>	<i>PIK3C2G</i>	PIK3CA Exons 2, 3, 5-8, 10, 14, 19, 21 (Coding Exons 1, 2, 4-7, 9, 13, 18, 20)	<i>PIK3CB</i>	<i>PIK3R1</i>	<i>PIM1</i>	<i>PMS2</i>	<i>POLD1</i>
<i>POLE</i>	<i>PPARG</i>	<i>PPP2R1A</i>	<i>PPP2R2A</i>	<i>PRDM1</i>	<i>PRKAR1A</i>	<i>PRKCI</i>	<i>PRKN</i> (PARK2)	<i>PTCH1</i>
PTEN	PTPN11	<i>PTPRO</i>	<i>QKI</i>	<i>RAC1</i>	<i>RAD21</i>	<i>RAD51</i>	<i>RAD51B</i>	<i>RAD51C</i>
<i>RAD51D</i>	<i>RAD52</i>	<i>RAD54L</i>	RAF1 Exons 3, 4, 6, 7, 10, 14, 15, 17, Introns 4-8	<i>RARA</i> Intron 2	RB1	<i>RBM10</i>	<i>REL</i>	RET Introns 7, 8, Exons 11, 13-16, Introns 9-11
<i>RICTOR</i>	<i>RNF43</i>	ROS1 Exons 31, 36-38, 40, Introns 31-35	<i>RPTOR</i>	<i>RSP02*</i> Intron 1	<i>SDC4*</i> Intron 2	<i>SDHA</i>	<i>SDHB</i>	<i>SDHC</i>
<i>SDHD</i>	<i>SETD2</i>	<i>SF3B1</i>	<i>SGK1</i>	<i>SLC34A2*</i> Intron 4	<i>SMAD2</i>	<i>SMAD4</i>	<i>SMARCA4</i>	<i>SMARCB1</i>
SMO	<i>SNCAIP</i>	<i>SOCs1</i>	<i>SOX2</i>	<i>SOX9</i>	<i>SPEN</i>	<i>SPOP</i>	<i>SRC</i>	<i>STAG2</i>
<i>STAT3</i>	STK11	<i>SUFU</i>	<i>SYK</i>	<i>TBX3</i>	<i>TEK</i>	<i>TENT5C</i> (FAM46C)	<i>TERC*</i> ncRNA	TERT* Promoter
<i>TET2</i>	<i>TGFBR2</i>	<i>TIPARP</i>	<i>TMPRSS2*</i> Introns 1-3	<i>TNFAIP3</i>	<i>TNFRSF14</i>	TP53	<i>TSC1</i>	<i>TSC2</i>
<i>TYRO3</i>	<i>U2AF1</i>	VEGFA	<i>VHL</i>	<i>WT1</i>	<i>XPO1</i>	<i>XRCC2</i>	<i>ZNF217</i>	<i>ZNF703</i>